

3101

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
9 August 2001 (09.08.2001)

PCT

(10) International Publication Number
WO 01/57270 A2

(51) International Patent Classification⁷: C12Q 1/68,
G06F 19/00, C07K 14/47

94043 (US). RANK, David, R. [US/US]; 117 El Dorado
Commons, Fremont, CA 94539 (US).

(21) International Application Number: PCT/US01/00661

(74) Agent: RONNING, Royal, N., Jr.; Amersham Pharma-
cia Biotech, Inc., 800 Centennial Avenue, Piscataway, NJ
08855 (US).

(22) International Filing Date: 29 January 2001 (29.01.2001)

(25) Filing Language: English

(81) Designated States (national): AE, A, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, H, CN, CR, CU, CZ,
DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(26) Publication Language: English

(30) Priority Data:		
60/180,312	4 February 2000 (04.02.2000)	US
60/207,456	26 May 2000 (26.05.2000)	US
09/608,408	30 June 2000 (30.06.2000)	US
09/632,366	3 August 2000 (03.08.2000)	US
60/234,687	21 September 2000 (21.09.2000)	US
60/236,359	27 September 2000 (27.09.2000)	US
0024263.6	4 October 2000 (04.10.2000)	GB

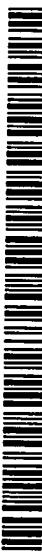
(84) Designated States (regional): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF,
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

(71) Applicant (for all designated States except US): MOLEC-
ULAR DYNAMICS, INC. |—/US; 928 East Arques Av-
enue, Sunnyvale, CA 94086 (US).

Published:

— without international search report and to be republished
upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.



WO 01/57270 A2

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE
EXPRESSION IN HUMAN BREAST AND HBL 100 CELLS

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene
expression in a sample derived from human HBL 100 cells is described. Also described are single exon nucleic acid probes expressed
in the HBL 100 cells and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BREAST AND HBL 100
CELLS

5 CROSS REFERENCE TO RELATED APPLICATIONS

The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the 10 benefit under 35 U.S.C. s 119(e) of U.S. provisional patent application serial nos. 60/236,359, filed September 27, 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of 15 UK patent application no. 0024263.6, filed October 4, 2000, the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
20 REFERENCE THEREOF

The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in 25 triplicate, containing a file named pto_HBL100.txt, created 24 January 2001, having 11,029,597 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

30 Field of the Invention

The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In 35 particular, the present invention relates to unique genome-

derived single exon nucleic acid probes expressed in human HBL 100 cells and single exon nucleic acid microarrays that include such probes.

5 Background of the Invention

For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to further the understanding of proteins – known or suspected – about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had 10 been both informed and directed by that antecedent 15 biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane 20 association, and by the predicted assembly of its gene via T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

25 More recently, however, the development of high throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes 30 understanding of the basic biology of the encoded protein product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences – that is, those accessible through isolation of 35 mRNA – are of greatest initial interest. This "expressed

sequence tag" ("EST") approach has already yielded vast amounts of sequence data (see for example Adams et al., *Science* 252:1651 (1991); Williamson, *Drug Discov. Today* 4:115 (1999)). For nucleic acids sequenced by this 5 approach, often the only biological information that is known *a priori* with any certainty is the likelihood of biologic expression itself. By virtue of the species and tissue from which the mRNA had originally been obtained, most such sequences are also annotated with the identity of 10 the species and at least one tissue in which expression appears likely.

More recently, the pace of genomic sequencing has accelerated dramatically. When genomic DNA serves as the initial substrate for sequencing efforts, expression cannot 15 be presumed; often the only *a priori* biological information about the sequence includes the species and chromosome (and perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence accumulation by directed, EST, and genomic sequencing 20 approaches – and in particular, with the accumulation of sequence information from multiple genera, from multiple species within genera, and from multiple individuals within a species – there is an increasing need for methods that rapidly and effectively permit the functions of nucleic 25 sequences to be elucidated. And as such functional information accumulates, there is a further need for methods of storing such functional information in meaningful and useful relationship to the sequence itself; that is, there is an increasing need for means and 30 apparatus for annotating raw sequence data with known or predicted functional information.

Although the increase in the pace of genomic sequencing is due in large part to technological changes in sequencing strategies and instrumentation, Service, *Science* 35 280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),

there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears 5 the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found 10 by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST 15 sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of 20 the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and 25 most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function 30 difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., 35 *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et

al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al., *Ismb* 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, 5 however, to give high false positive rates. Burset et al., *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence.

Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

10 Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may 15 need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the 20 expression of regions predicted to encode protein - readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in 25 Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books 30 Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or 35 from the construction of "problem specific" libraries

targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes 5 for genes discovered solely by genomic sequencing.

The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of 10 yeast nuclear genes, approximately 95% however, are single exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally 15 been used to probe gene expression from more complex eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the breast are a significant cause of human morbidity and mortality. Increasingly, genetic 20 factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the breast, for the most part these disorders are believed to have 25 polygenic etiologies. There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the human breast, particularly those diseases with polygenic etiology.

30 Summary of the Invention

The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional 35 information derived from genomic sequence. The present

invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

5 In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

10 The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

15 Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human Breast, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 5,074 or a complementary sequence, or a portion of such a sequence.

20 By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

25 In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

30 In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

35 In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 10,058 or a complimentary sequence, or a 5 portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, 10 preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 15 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

25 Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane 30 which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, 35 polyacrylate, polymethylmethacrylate, polyvinylchloride,

polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

5 In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

10 In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of 15 amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

15 In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon 20 probes that include specifically-hybridizable fragments of SEQ ID Nos. 5,075 - 10,058, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 5,074.

25 Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human Breast which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 30 5,074 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Breast.

35 In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.: 5,075

- 10,058 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human Breast 5 which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOS.: 10,059 - 15,009 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Breast.

10 Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, 15 suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

20 In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

25 Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

30 In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 35 and Cy5 although other suitable dyes will be known to those

skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and 5 bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is 10 provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

15 wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human Breast, comprising:

20 contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human Breast; and then

25 measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

30 algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

35 wherein said detectably labeled nucleic acids are derived from mRNA from the Breast of said eukaryote, said

probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the 5 invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

10 identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using 15 hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single 20 gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 10,058 wherein said sequence encodes a peptide.

25 In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 5,075 - 10,058, or a complementary sequence or coding portion thereof.

30 In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 - 5,074.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 10,059 - 15,009.

35 Accordingly in a eleventh aspect of the invention

there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 10,059 - 15,009, or fragment thereof.

In another aspect, the invention provides means 5 for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated 10 sequence.

Detailed Description of the Invention

15 Definitions.

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately 20 detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach 25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1) (suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the 30 term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner 35 et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000);

in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid 5 microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution 10 phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the 15 sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop 25 codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the 30 consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a 35

sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.:. The codons 5 encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a 10 nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present 15 within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is 20 meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , 25 preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display 30 of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

35 As used herein, a "Mondrian" means a visual

display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

5

Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and 10 examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in 15 meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

20 FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

25 FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

30 FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

35 FIG. 7 is a pictorial representation of the

expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured 5 tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

10 FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a 15 BLAST Expect ("E") value of greater than 1e-30 (1×10^{-30}) . ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than 1e-30 (1×10^{-30}) ("known");

20 FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

25 Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

30 FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original 35 sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than

human, such as mouse, rat, Arabidopsis, *C. elegans*, *C. briggsii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

5 Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, 10 encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing 15 somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

 The particular genomic sequence to be input into process 200 will depend upon the function for which 20 relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

25 Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic 30 assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

35 The subset of sequences output from process 300

is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

5 Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by
10 incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for
15 incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

20 The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magneto-optical disk, flash memory, or the like.

25 FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational
30 substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.
35 Often, data will be stored after each, or at least a

plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to 5 process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be 10 identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction 15 analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of 20 sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend 25 upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the 30 sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that 35 compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently 5 long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment 10 length, such as 10 kb, more typically 20 kb, 30 kb, 40 kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal 15 number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes 20 (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate 25 a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been 30 described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is 35 possible to query the database for newly added sequence,

either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, 5 temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts 10 that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST 15 and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

20 If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the 25 database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to 30 report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional 35 preprocessing 24, suitable and specific for the desired

analytical approach and the particular analytical methods thereof to be used in process 25.

5 Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis.

10 Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

15 Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using 20 programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified 25 algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can 30 be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the 35 undesired sequence as, for example, by converting the

specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, 5 leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered 10 occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

15 Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived 20 from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the 25 input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, 30 where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after 35 transcription into mRNA, regulating message splicing after

transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X 5 chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, 10 for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described 15 become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene 20 prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and 25 GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For 30 the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 35 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase 5 reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

10 Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to 15 process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report 20 consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% 25 of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

30 Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process 35 can be repeated on the same input sequence, or subset

thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, 5 but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done 10 in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional 15 assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental 20 verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the 25 species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

30 Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify 35 and select those ORFs that appear most likely successfully

to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that 5 subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, 10 reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

15 The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

20 As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The 25 combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In 30 particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

35 Putative ORFs as predicted by a consensus of gene

calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is 5 conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) 10 sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500 15 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more 20 effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 25 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs 30 predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at 35 amplifying pieces of such ORFs is low, and that such

putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

5 The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no 10 more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

15 Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit 20 further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all 25 amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not 30 exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from 35 which the genomic sequence data had originally been

obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology 5 : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 10 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material 15 flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the 20 absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial 25 advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support 30 substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

35 Typically, the support substrate will be glass,

although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 5 polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even 10 spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached 15 covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

20 Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources 25 (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays 30 typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or 35 32 *E. coli* genes suffice to provide a robust measure of

background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural 5 nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the 10 immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates, 15 the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

20 For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using 25 nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid 30 probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For 35 example, each standard microscope slide can include at

least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

5 Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as 10 is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

15 The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) 20 those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, 25 it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, 30 R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, 35 shown herein to represent only a fraction of expressed

genes. Furthermore, such libraries – and thus microarrays based thereupon – are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message 5 successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined – subsequently arrayed for expression 10 measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention – that is, the one third of sequences 15 that had previously been accessioned in EST or other expression databases – are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, 20 optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor 25 cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from 30 genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST 35 approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

5 As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a 10 spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention 15 lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, 20 where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical 25 derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the 30 probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from 35 genomic DNA. Typically, therefore, at least about 50, 60,

70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage.

5 Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including 10 probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

15 As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes 20 disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific 25 primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the 30 genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even 35 smaller amount of nonspecific sequence that would

contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the

present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

5 Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization 10 results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (i.e., mismatched) sequence.

15 In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 20 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

25 A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound 30 noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large 35 percentage differences in the theoretically optimum

stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the 5 range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the 10 quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present 15 substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* — that is, only about 4 20 - 5% — have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons 25 on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm 30 expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% 35 of protein-encoding genes have introns. In preferred

embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about 5 one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present 10 invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, 15 through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA 20 sources, according to techniques well known in the microarray art, *Reviewed in Schena et al.*, and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single 25 cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased 30 commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a 35 fluorophore (fluorochrome; fluor; fluorescent dye); the

reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes 5 prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned 10 using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

15 Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for 20 subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

25 Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

30 In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher 35 density arrays, such as are provided by microtiter plates

media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in 5 international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should 10 be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and 15 characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic 20 sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected 25 of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, 30 SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query - 35 including information on identical sequences and

information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence – can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, 5 process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such 10 annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or 15 by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

20 The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the 25 information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively 30 described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an 35 annotated sequence, representation of individual

nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention 5 herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian 10 visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of 15 rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, 20 as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession 25 number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is 30 anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual 35 display 80 is used as a graphical user interface to

computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

5 Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle
10 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach
15 identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of
20 horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the
25 functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or
30 approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from
35 GRAIL or GRAIL II, rectangles 83b can represent the results

from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method 5 and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to 10 report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where 15 display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by 20 pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 25 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as 30 many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. 35 However, the increased visual complexity occasioned by such

display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-
5 selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted 10 functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the 15 results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function 20 by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is 25 protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe 30 immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

35 Rectangle 87 is used to present the results of

bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as

can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of 5 expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which 10 often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right 15 borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical 20 assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, 25 individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the 30 spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such 35 relative expression (expression ratios) and absolute

expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

30 Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present

invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of 5 single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present 10 invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon 15 microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 5,074 of these ORFs in HBL 100 cells.

20 The HBL 100 human breast cancer cell line was established in vitro from milk of an apparently healthy woman. The cells express a variant of SV40 large T antigen, and genomic DNA from HBL 100 cells possesses transforming activity associated with the viral 25 information. The HBL100 cell line is nontumorigenic, and acquires the capacity to invade normal tissues and to replace them by proliferation in vitro only at high passage levels (HPL); these epithelial cells are thus are a useful model for studying breast tumor progression in vitro. HBL 30 100 cells bind both epidermal growth factor (EGF) and glucocorticoids but are progesterone receptor negative.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in HBL 100 cells is currently available for use 35 in measuring the level of its ORF's expression in Breast.

Diseases of the breast are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the breast, for the most part these disorders are believed to have polygenic etiologies.

For example, according to the American Cancer Society (ACS), carcinoma of the breast is the second most common cancer in women and, after lung cancer, is the second deadliest. The ACS estimates that in the U.S. there occurred 182,800 new cases of malignant breast cancer in 2000, and about 40,800 deaths from the disease. Although incidence of breast cancer is said to have declined, the disease clearly continues to represent a serious risk to the health and life of American women. Indeed, about one in nine U.S. women will develop breast cancer in her lifetime, and at present mortality rates, about a third of such women will eventually die from the disease.

A variety of factors are known to increase the risk of breast carcinoma. Sex is one: breast cancer in men is rare. Age is another: as women age, their risk for developing breast cancer increases, a 70 year old woman having three times the risk of developing cancer and five times the risk of dying from the disease as compared to a 40 year old woman. Most breast cancers occur after age 50, although in women with a genetic susceptibility, breast cancer tends to occur at an earlier age than in sporadic cases. Reproductive and menstrual history are also known to affect risk, with risk increasing with early menarche and late menopause, and is reduced by early first full term pregnancy. Additional risk factors, oft-times termed "lifestyle factors", include weight gain, obesity, fat intake, alcohol consumption, and level of physical

activity.

That genetic factors underlie the etiology of breast cancer is suggested by the approximately two-fold increased risk for development of breast cancer by women 5 with a first-degree relative who has also developed breast cancer. After gender and age, a positive family history is the strongest known predictive risk factor for breast cancer. Genetic linkage analysis in families with high rates of inherited cancer have facilitated the 10 identification of several genes in which mutations can be shown to contribute substantially to the development and progression of breast cancer, including BRCA1, BRCA2, p53, and PTEN/MMAC1. Further study has made clear, however, that these genes are not alone sufficient to explain all 15 genetic contributions to breast cancer.

For example, BRCA1 appears to be responsible for disease in up to 90% of families with both breast and ovarian cancer, but in only 45% of families with multiple cases of breast cancer without occurrence of ovarian 20 cancer. And mutations in BRCA2, localized to the long arm of chromosome 13, are thought to account for only approximately 35% of multiple case breast cancer families. Furthermore, despite the strong correlation between 25 germline mutations in BRCA1 or BRCA2 and development of breast cancer, only weak connections have been made between these genes and sporadic breast cancer.

Epistatic effects of BRCA1 and BRCA2 mutations on other genetic loci, only some of which have been identified, have been postulated to account for some of the 30 deleterious effects of mutations in these two genes.

Thus, mutations in p53 seem to be much more frequent in BRCA1 breast cancers (20/26) and somewhat more frequent in BRCA2-associated breast cancers (10/22) than in grade-matched sporadic cancers (7/20). BRCA mutation- 35 associated cancers contain p53 mutations not typically

found in sporadic breast cancer, and 12 individual hereditary breast cancers have been shown to contain more than a single p53 mutation. Mutations of BRCA1 and BRCA2 may thus confer a "mutator" phenotype permitting the 5 accumulation of genetic abnormalities, with p53 inactivation selected during tumor progression.

Additionally, genome-wide screening for chromosomal gains or losses in breast cancers harboring BRCA1 or BRCA2 mutations demonstrated more regions that 10 were amplified or deleted compared to controls, suggesting a generalized increase in large-scale genomic instability. Chromosomes 5q, 4q, and 4p had very frequent loss of heterozygosity in BRCA1 tumors, while BRCA2 tumors were characterized by losses at 13q (near the BRCA2 locus 15 itself) and 6q, and chromosomal gains at 17q (outside of the HER2/neu locus) and 20q.

Mutations of other genes have also been implicated in susceptibility to development or aggressiveness of breast cancer. For example, germline 20 mutations in the ATM gene, localized to chromosome 11q22-23, result in an increased risk of breast cancer among female heterozygote carriers with an estimated relative risk of 3.9 to 6.4; it is unclear, however, if mutations in the ATM gene itself contribute to breast 25 cancer.

Normal allelic variation in a variety of genes, as opposed to frank mutation, may also influence susceptibility to developing breast carcinoma and the propensity for the disease to progress. Such 30 polymorphisms may thus explain why particular women or ethnic groups who do not otherwise bear mutations in genes known to be linked to breast cancer are at greater risk, especially in the context of exposure to environmental agents and other nonhereditary risk factors.

35 Polymorphically expressed genes may code for enzymes that

metabolize estrogens or detoxify drugs and environmental carcinogens.

For example, molecular epidemiologic studies of cancer of the breast have examined associations with p450 5 cytochrome genotypes including CYP1A1, CYP2D6, and CYP17. The CYP1A1 gene, located on chromosome 15q, encodes the enzyme aryl hydrocarbon hydroxylase (AHH), present in breast tissue, and which catabolizes polycyclic aromatic hydrocarbons and arylamines. AHH is strongly inducible, 10 i.e., greater enzymatic activity is seen with greater exposure to substrates. AHH catalyzes the monooxygenation of polycyclic aromatic hydrocarbons to phenolic products and epoxides that may be carcinogenic. AHH is also involved in the conversion of estrogen to hydroxylated 15 conjugated estrogens such as 2-hydroxyestradiol.

Three polymorphisms in the CYP1A1 gene have been identified: an MspI RFLP of the 3' end of the gene (MspI); an adenine to guanine mutation in exon 7, causing an isoleucine to valine substitution (Ile-Val); and a 20 polymorphism of the CYP1A1 gene identified among Negroids. The frequencies of the MspI and Ile-Val polymorphisms vary considerably by race, being higher among Japanese and Hawaiian populations as compared with Caucasians and Negroids.

25 The CYP2D6 gene is located on chromosome 22q and encodes the enzyme debrisoquine hydroxylase, which metabolizes a variety of drugs and other xenobiotics. Like other polymorphically expressed p450 enzymes, it may activate procarcinogens or, conversely, detoxify 30 carcinogens. A number of alleles have been characterized at the CYP2D6 locus. The "poor metabolizer" phenotype (CYP2D6 mutant/mutant genotype), which is rare in Asians, occurs in about 5% to 10% of Caucasians and in 2% of Negroids.

35 As another example, the N-acetyl transferase-1

(NAT1) and N-acetyl transferase-2 (NAT2) genes are located on chromosome 8q. Allelic variation in the NAT genes may contribute to variation in populations as to the susceptibility of individuals to development of breast carcinoma, particularly in the context of exposure to compounds present in tobacco. NAT2 detoxifies or, conversely, activates aromatic amines found in tobacco smoke such as 4-aminobiphenyl. Both phenotypic assays and genotypic assays for NAT2 can be used to classify individuals as rapid or slow acetylators. Genetic variants of the NAT2 gene have been cloned and 6 alleles at this locus have been identified: the F1 allele confers the fast acetylator phenotype. The distribution of NAT1 and NAT2 alleles differs widely between racial and ethnic groups.

As yet another example, the glutathione S-transferase-M1 (GSTM1) gene is located on chromosome 1 and the gene for glutathione S-transferase-T1 (GSTT1) is located on chromosome 11q. A glutathione S-transferase-P1 (GSTP1) gene has also been identified.

Glutathione S-transferases detoxify a variety of carcinogens and cytotoxic drugs (for example, benzo(a)pyrene, monohalomethanes such as methyl chloride, ethylene oxide, pesticides, and solvents used in industry) by catalyzing the conjugation of a glutathione moiety to the substrate. Allelic variation in the glutathione-S-transferase genes may contribute to variation in populations as to the susceptibility of individuals to development of breast carcinoma, particularly in the context of exposure to environmental toxins. Individuals homozygous for deletions in the GSTM1, GSTT1, or GSTP1 genes may have a higher risk of cancer of the breast and other sites because of their impaired ability to metabolize and eliminate carcinogens.

GSTM1 is polymorphically expressed and 3 alleles at the GSTM1 locus have been identified: GSTM1-0

12q22-q24.1; IGF1R (JTK13) 15q25-q26; IGF2
11p15.5; IL6 (IFNB2) 7p21; ING1 13q34; KISS1 (KiSS-1) 1q32;
KLK3 (PSA, APS) 19q13; LASP1 (MLN50) 17q11-q21.3; LIBC
6q22; MAP2K4 (MKK4, SEK1, JNKK1) 17p11.2; MKI67 (Ki-67)
5 10q25-qter; MMP11 (STMY3, STR3) 22q11.2; MMP2 (CLG4A, CLG4,
GELA) 16q13; MUC1 (PUM, PEM) 1q21; MYC (CMYC, C-MYC)
8q24.12-q24.13; NOTCH4 (INT3, NOTCH3) 6p21.3; PCNA 20p12;
PI5 (maspin) 18q21.3; PLAU (uPA, URK) 10q24; PSEN2
(D21S21, HPS2, BCEI) 21q22.3; RARB (NR1B2, HAP) 3p24; RB1
10 (Rb) 13q14.2; S100A4 (MTS1, P9KA, metastasin) 1q21;
SLC22A1L (BWSR1A, ORCTL2, IMPT1) 11p15.5; SNCG (BCSG1)
10q23.2-q23.3; SRD5A2 2p23; STIP1 (HSP70) 11?; STK11 (LKB1,
PJS) 19p13.3; TFAP2A (AP2, AP2TF) 6p24; TFAP2B (AP2B)
6p12; TFAP2C 20q13.2; TFF1 (D21S21, BCEI) 21q22.3; TGFBR2
15 3p22; TIMP2 17q25; TP53 (p53, P53) 17q13.1; TPD52 (D52)
8q21; TPD52L1 (D53, hD53) 6q22-q23; TSG101 11p15.2-p15.1.

The etiology of non-cancerous disorders of the breast may also involve genetic factors. Such disorders include disorders of development, inflammatory diseases of 20 the breast, fibrocystic changes, proliferative breast disease, and non-carcinoma tumors.

Disorders of development of the breast include supernumerary nipples or breasts; accessory axillary breast tissue; congenital inversion of the nipples; and 25 macromastia.

Inflammatory diseases of the breast include acute mastitis; periductal mastitis, also called recurrent subareolar abscess and squamous metaplasia of the lactiferous ducts; mammary duct ectasia; fat necrosis; and 30 granulomatous mastitis, including granulomatous lobular mastitis. Systemic granulomatous diseases that can affect the breast include Wegener granulomatosis and sarcoidosis.

Proliferative breast diseases include epithelial hyperplasia; sclerosing adenosis; and small duct 35 papillomas. Non-carcinoma tumors include stomal tumors

including fibroadenoma and phyllodes tumor, and sarcomas that include angiosarcoma, rhabdomyosarcoma, liposarcoma, leiomyosarcoma, chondrosarcoma and osteosarcoma. Other breast tumors include epithelial cell tumors including 5 large duct papillomas.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human breast, particularly those 10 diseases with polygenic etiology. With each of the single exon probes described herein shown to be expressed at detectable levels in human breast cancer cells, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide 15 exceptionally high informational content for such studies.

For example, diagnosis, grading, and/or staging of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known to be characteristic of 20 a given breast disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the 25 patient's breast to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from individuals with known disease. Methods for quantitatively relating gene expression profiles, without regard to the . 30 function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be 35 used to interrogate genomic DNA, rather than pools of

expressed message; this latter approach permits predisposition to and/or prognosis of breast disease to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's 5 genome of exons known to be expressed in human breast. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at 10 sufficiently high hybridization stringency, which stringencies are well known in the art - see Ausubel et al. and Maniatis et al. - each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the 15 probes of the present invention, for which expression in the HBL 100 cells has been demonstrated are useful for both measurement in the Breast and for survey of expression in other tissues.

Significant among such advantages is the presence 20 of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which 25 the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of 30 only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

35 Either as tools for measuring gene expression or

tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

5 The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

10 Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

15 Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell 20 Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); 25 Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

30 Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for

example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., 5 "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and 10 Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the 15 Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

20 In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, 25 serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway 30 of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents – whether in lead compound discovery or in subsequent screening of lead compound derivatives – the inability of the agent to alter 35 a gene's expression level is evidence that the drug does

not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

10 Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

15 The invention particularly provides genome-derived single-exon probes known to be expressed in HBL 100 cells. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

20 Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules 25 so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are 30 described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

35 Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the

hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to 5 PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are to be provided in a form suitable for amplification, the 10 range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be 15 sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be 20 packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first 25 common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe 30 composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the 35 present invention will typically average at least about

100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the 5 genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a hybridization reaction in which the probe is not first 10 bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that 15 dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human 20 genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention 25 can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 5,075 - 10,058, respectively, for probe SEQ ID NOS. 1 - 5,074. The minimum amount of ORF required to be included in the probe of the present invention in order to 30 provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 5,075 - 10,058 individually by routine experimentation using standard high stringency conditions.

35 Such high stringency conditions are described.

inter alia, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human *cot1* DNA, and 0.5 % SDS, in a 5 humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization 10 at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room 15 temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single 20 exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more 25 than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more 30 than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well 35 understood by one of skill in the art, single stranded

probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in 5 both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and 10 below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that 15 the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can 20 usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR®

Green and other labels described in Haugland, 25 *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for 30 ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be 35 provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural 5 individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

10 If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 15 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human HBL 100 20 cells.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

25 The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid 30 amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays 35 useful for gene expression analysis, where the term

"microarray" has the meaning given in the "definitional" section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human HBL 100 cells. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 5,074.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue.

At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 5,074 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 5,075 - 10,058, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 5,074 can be used, or that portion thereof in SEQ ID NOS. 5,075 - 10,058

used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially 5 that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT™ Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, inter 15 alia, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7), Oxford Univ. Press 20 (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence 25 translated from SEQ ID NOS.: 5,075 - 10,058. Such amino acid sequences are set out in SEQ ID NOS: 10,059 - 15,009. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate 30 antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted
5 in Human Genomic Sequence

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces
that had been accessioned in a five month period
10 immediately preceding this study were downloaded from
GenBank. This corresponds to ~2200 clones, totaling ~350
MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the
program CROSS_MATCH, the sequence was analyzed for open
15 reading frames using three separate gene finding programs.
The three programs predict genes using independent
algorithmic methods developed on independent training sets:
GRAIL uses a neural network, GENEFINDER uses a hidden
Markoff model, and DICTION, a program proprietary to
20 Genetics Institute, operates according to a different
heuristic. The results of all three programs were used to
create a prediction matrix across the segment of genomic
DNA.

The three gene finding programs yielded a range
25 of results. GRAIL identified the greatest percentage of
genomic sequence as putative coding region, 2% of the data
analyzed. GENEFINDER was second, calling 1%, and DICTION
yielded the least putative coding region, with 0.8% of
genomic sequence called as coding region.

30 The consensus data were as follows. GRAIL and
GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and
DICTION agreed on 0.5% of genomic sequence, and the three
programs together agreed on 0.25% of the data analyzed.
That is, 0.25% of the genomic sequence was identified by
35 all three of the programs as containing putative coding

region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

10

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant

further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon 5 to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR® 10 green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

15 The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue 20 (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR 25 amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 30 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of 35 successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less

than $1 e^{-100}$) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from $1 e^{-5}$ to $1 e^{-99}$). The remaining 45% of 5 the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt 10 database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

15

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 15 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in 20 each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 μ g of polyA⁺ mRNA performed using 1 μ g oligo(dT)12-18 primer and 2 μ g random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After 30 snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100 μ M dATP, 100 μ M dGTP, 100 μ M dTTP, 50 μ M dCTP, 50 μ M Cy3-dCTP or Cy5-dCTP 50 μ M, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. 35 After 2 hours, the first strand cDNA was isolated by adding

1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

5 Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_{ot}1 DNA, and 0.5 % SDS.

10 Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% 15 SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

20 Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, 25 since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, 30 "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

35 Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by

the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

5 FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues
10 tested ("10").

15 Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single
20 tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

25 FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the
30 respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using
35 the probe sequence. The legend for "bioinformatic"

expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

5 As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were 10 identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

15 It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate 20 of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes 25 expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

Comparison of Signal from Known and Unknown Genes

30 The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

35 FIG. 8 shows the normalized Cy3 signal intensity

for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all 5 sequence-verified products with a BLAST Expect value of less than 1e-30 ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the 10 ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large 15 number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA 20 library.

The significant point is that presence of the gene in an EST database is *not* a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to 25 assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic 30 sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific 35 gene expression patterns as measured by the microarray

experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, 5 Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two 10 sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and 15 indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in 20 expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

25 To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed 30 high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences 35 showing the highest signal in brain in microarray

hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca^{2+} binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding

				protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter

confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the 5 gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097 (1997).

A number of the brain-specific probe sequences 10 (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 15 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in 20 this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common 25 genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were 30 found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

35 Other interesting genes highly expressed in brain

were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip 5 sequences included a translation elongation factor 10 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., *Genomics* 49(2):283-89 (1998)) (AC007320-3). A low homology analog 10 (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature 15 (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. 15 This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 20 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

25 Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0.05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	-1.41 ± 0.05
HBL100	1.32 ± 0.05	2.64 ± 0.12

Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ± 0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±
Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again 5 demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray 10 experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15 For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding 20 programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual 25 display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

30 FIG. 9 presents a Mondrian of BAC AC008172 (bases

25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

5 As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTIION identified 7 of the known exons (19%).

10 Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

15 The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We 20 selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression 25 patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they 30 show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom): red = kallistatin protease inhibitor (P29622); purple = plasma serine protease inhibitor (P05154); 35 turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S

ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

5 EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

The protocols set forth in Examples 1 and 2, 10 supra, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in HBL 100 cells.

These unique exons are within longer probe 15 sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base- 20 incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented 25 fragments of each of the 5,074 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

The structures of the 5,074 unique single exon probes are clearly presented in the Sequence Listing as SEQ 30 ID Nos.: 1 - 5,074. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 5,075 - 10,058, 35 respectively. It will be noted that some amplicons have

more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon 5 probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed 10 from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is 15 determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the 20 duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than 25 median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified 30 control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

35 This means that, assuming that the data is

distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5.

5 Example 5 presents the subset of probes that is significantly expressed in the human HBL 100 cells and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human HBL 100 cells.

10 The sequence of each of the exon probes identified by SEQ ID NOS.: 5,075 - 10,058 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because 15 the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the 20 three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were 25 found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe: "EXON SEQ ID NO.:") from least similar to sequences known to be 30 expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, 35 the accession number of the database sequence that yielded

the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

5 corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS... The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn 10 from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts 15 with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 20 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried 25 databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences 30 (e.g., those with BLAST E values between about 1e-05 and 1e-100), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of 1e-05 (i.e., 1 x 10⁻⁵) and 1e-100 (i.e., 1 x 10⁻¹⁰⁰) as evidence of similarity 35 to sequences known to be expressed is of course arbitrary:

in Example 2, *supra*, a BLAST E value of 1e-30 was used as the boundary when only two classes were to be defined for analysis (unknown, >1e-30; known <1e-30) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E 5 Value" is low, e.g., less than about 1e-100 - which is probative evidence that the query sequence has previously been shown to be expressed - the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not 10 have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, 15 without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOS.: 1 - 5,074) and probe exon (SEQ ID NOS.: 5,075 - 10,058, 20 respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about 25 the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST 30 query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5Genome-Derived Single Exon Probes Useful For Measuring
Expression of Genes in Human HBL 100 cells

5

Table 4 (209 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human HBL 100 cells, a hormone sensitive human breast cancer cell line.

10

Page 1 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
447	5484	10501		4.37			
878	6596	10537		8.5			
1028	6038			2.62			
1283	6282	11324		8.84			
1577	6574	11636		3.1			
1656	6592	11653		4.71			
1887	6683	11758		2.18			
1710	6705	11781		1.16			
1717	6712	11789		7.06			
1850	6839	11828		1.12			
1833	6919	12018		1.75			
2101	7082	12197		1.88			
2216	7193	12315		4.79			
3112	8128	13148		3.32			
3366	8374	13394		1.09			
3437	8445	13471		12.48			
3481	8489			1.38			
3573	8573	13588		1.16			
3844	8848			1.1			
4074	9068	14058		1.73			
4139	9134	14117		6.13			
4211	9204			1.28			
4689	9874	14867		1.1			
4878	9858	14829		4.14			
4888	8867	14837		1.25			
2595	7558	12872		0.93	9.4E+00	L111433.1	NT
2695	7558	12873		0.93	9.4E+00	L11433.1	NT
2863	7873	12888		3.02	9.4E+00	AB043785.1	NT
437	5475	10491		2.23	8.4E+00	6031804	NT
2809	7928	12946		3.48	7.2E+00	L12051.1	NT
2809	7928	12947		3.48	7.2E+00	L12051.1	NT
3445	8453			0.71	6.8E+00	7661557	NT

Dengue virus type 3 membrane protein (pNM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
 Dengue virus type 3 membrane protein (pNM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
 Mus musculus AT3 gene for anilirhabdin, complete cds
 Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
 Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds
 Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds
 Homo sapiens DESC1 protein (DESC1), mRNA

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4840 8825	14617	1.32	5.3E+00	L49128.1	NT		Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
3949 8947		11.08	4.8E+00	AF185255.1	NT		Eunice austriatilis histone H3 (H3) gene, partial cds
287 5345	10357	2.26	4.7E+00	BF240552.1	EST_HUMAN	601875654F11 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089716 5'	
288 5345	10357	1.89	4.7E+00	BF240552.1	EST_HUMAN	601875654F11 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089716 5'	
3200 8216	13237	1.53	4.7E+00	AL163280.2	NT		Homo sapiens chromosome 21 segment HS21C080
3469 8477		1.24	4.0E+00	P38229	SWISSPROT		GLC7-INTERACTING PROTEIN 1
3124 8432	13458	4.3	3.8E+00	X64518.1	NT		Naibacum chitinase gene 50 for class I chitinase C
4194 9187		0.7	3.9E+00	AF054661.1	NT		Mus musculus seminal vesicle secretory protein 98 (MSVSP98) gene, promoter region
2857 7522		1.48	3.8E+00	AE001562.1	NT		Helicobacter pylori, strain J98 section 123 of 132 of the complete genome
3912 8912	13807	11.92	3.7E+00	AL161539.2	NT		Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
5050 10021		1.5	3.7E+00	AF216280.1	NT		Mus musculus heterochromatin protein 1 alpha mRNA, complete cds
588 5619	10617	3.88	3.6E+00	AV761056.1	EST_HUMAN	AV781056 MDS Homo sapiens cDNA clone MDSB1E10 5'	
3174 8190	13211	0.95	3.5E+00	AF221538.1	NT		Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
1481 8478	11634	2.28	3.4E+00	AF254577.1	NT		Brassica napus RPB5d mRNA, complete cds
497 6533	10540	1.62	3.2E+00	X98422.1	NT		Danio rerio zp-50 POU gene
4588 9576	14587	1.44	3.2E+00				Homo sapiens carcinomaembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
2764 7786	12809	2.05	3.0E+00	4502404	NT		Homo sapiens hypothetical protein PRO0088 (PRO19589), mRNA
1981 6847	12049	1.8	2.9E+00	AE002235.2	NT		Chlamydomonas AR39, section 53 of 94 of the complete genome
1430 6427	11485	4.89	2.8E+00	AF186598.1	NT		Buxus harlandii maturase K (malk) gene, partial cds; chloroplast gene for chloroplast product
1593 6589		1.65	2.8E+00	AL161552.2	NT		Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
230 5293	10301	19.61	2.7E+00	6679306	NT		Mus musculus per-hexameric repeat gene 3 (Phnx3), mRNA
230 5293	10302	18.61	2.7E+00	6679308	NT		Mus musculus per-hexameric repeat gene 3 (Phnx3), mRNA
4538 9528	14514	5.79	2.6E+00	AF068749.1	NT		Mus musculus sphingosine kinase (SPHK16) mRNA, complete cds
1436 6433	14689	2.05	2.6E+00	A1271844.1	NT		Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
1438 6433	14490	2.05	2.5E+00	A1271844.1	NT		Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
2944 7983	12983	0.8	2.4E+00	M24282.1	NT		Chicken alpha-3 collagen type VI mRNA, 3' end
4752 9737	14723	5.52	2.4E+00	45033352	NT		Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
1234 6232	11276	13.73	2.3E+00	Z48724.1	NT		G. domesticus artificial single chain antibody gene (L3)
4002 8998		1.54	2.3E+00	A1401081.1	NT		Bos taurus partial cytb gene for cytochrome b
3910 8910	13906	1.11	2.2E+00	AF020288.1	NT		Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4188 9179	14162	4.09	2.2E+00	D67071.1	NT		Re1 gene for regulardin, exon 1 (non-coding exon)
4188 9179	14163	4.09	2.2E+00	D67071.1	NT		Re1 gene for regulardin, exon 1 (non-coding exon)
584 7724	10597	7.72	2.1E+00	AF32812.2	NT		Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region

Page 3 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2B48	7867	12985	1.2	2.1E+00	AF208532.1	NT	Human sapiens, fatty acid omega-hydroxylase CYP4A11 (CYP4A11) gene, complete cds
3507	65115		0.83	2.1E+00	AW449286.1	EST_HUMAN	U1-H-B13-ak1-e-08-0-U1-s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2731550 3'
1177	8179	11215	2.45	2.0E+00	AF180527.1	NT	Human sapiens P22Dok1a (DOKDEL) mRNA, complete cds
1177	6179	11216	2.45	2.0E+00	AF180527.1	NT	Human sapiens P22Dok1a (DOKDEL) mRNA, complete cds
1316	6312	11361	1.07	2.0E+00	AF204927.1	NT	Oryctodius cuniculus Na ⁺ -K ⁺ -ATPase beta 1 subunit mRNA, complete cds
1540	65338		3.99	2.0E+00	P25582	SWISSPROT	PUTATIVE RNA METHYLTRANSFERASE SPB1
2088	7069	12182	8.21	2.0E+00	Z78278.1	NT	R.norvegicus mRNA for collagen alpha1 type I
2088	7069	12183	8.21	2.0E+00	Z78278.1	NT	R.norvegicus mRNA for collagen alpha1 type I
3984	6982	13967	1.95	2.0E+00	AW684496.1	EST_HUMAN	h113c05.x1 NCI_CGAP_GU11 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
3984	6982	13968	1.95	2.0E+00	AW684496.1	EST_HUMAN	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN); h113c05.x1 NCI_CGAP_GU11 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
3019	80336	13046	1.75	1.8E+00	P21004	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN); PROTEIN B8 PRECURSOR
3047	8064	13072	2.44	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7912 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (alpE) genes, complete cds
3047	8064	13073	2.44	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7912 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (alpE) genes, complete cds
1091	6098	11127	1.85	1.7E+00	Q60114	SWISSPROT	LEAVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE-6-FRUCTOSYL TRANSFERASE)
2209	7188	12308	2.62	1.7E+00	AL1632380.2	NT	Human sapiens chromosome 21 segment HS1C080
2312	7287	12408	1.36	1.7E+00	AA141097.1	EST_HUMAN	oz43h05.x1 Scores_Nh1Mfu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
1983	69688	12074	8.04	1.6E+00	AF199339.1	NT	Human sapiens lens epithelial-derived growth factor gene, alternatively spliced, complete cds
1882	6977	12081	2.96	1.6E+00	AF077374.1	NT	Human sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
1896	6980	12035	1.09	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
2220	7197		4.52	1.6E+00	X88373.1	NT	B1nep gene encoding endo-polylacturonase
2891	7910	12931	1.57	1.6E+00	W58426.1	EST_HUMAN	z2d25f01.1 Scores_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb:D28805_N-ACETYLGLUCOSAMINE SYNTHASE (HUMAN);
3921	8921		5.49	1.6E+00	BF570977.1	EST_HUMAN	gb:D28805_N-ACETYLGLUCOSAMINE SYNTHASE (HUMAN); 60218608571 NIH_3T3 Homo sapiens cDNA clone IMAGE:4310591 3'
4226	9220	14199	1.68	1.6E+00	AF155827.1	NT	Human sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4226	9220	14200	1.88	1.6E+00	AF155827.1	NT	Human sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4911	8890	14863	2.77	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
4911	9890	14884	2.77	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
33	5113	10089	4.81	1.6E+00	U53448.1	NT	Rattus norvegicus jun dimerization protein 2 (Jdp-2) mRNA, complete cds
231	6294	10303	1.98	1.6E+00	AE002201.2	NT	Chlamydomonas reinhardtii AR38, section 32 of 94 of the complete genome

Page 4 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
616	5643			1.7	1.5E+00	6752861	NT
2344	7318	124338	1.68	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2444	7414	12530	1.67	1.6E+00	6875350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3095	7318	124338	2.59	1.6E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
30	5110	100985	1.17	1.4E+00	7681685	NT	Homo sapiens DKFZP886M0122 protein (DKFZP886M0122), mRNA
30	5110	100986	1.17	1.4E+00	7681685	NT	Homo sapiens DKFZP886M0122 protein (DKFZP886M0122), mRNA
2272	7248		7.96	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2568	7560	128777	1.44	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2701	7658	12771	3.21	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP8), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2701	7658	12772	3.21	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP8), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3259	8272		0.89	1.4E+00	5453733	NT	Homo sapiens Mad4 homolog (MAD4) mRNA
4453	9443		1.34	1.4E+00	BF681547.1	EST_HUMAN	60215668/F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'
4894	9966	14944	1.02	1.4E+00	BE972428.1	EST_HUMAN	601652250/F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:393556 5'
565	5598		1.44	1.3E+00	Z73640.1	NT	M.mucedo gene encoding 4-Dihydroxy-3-isopropylidene dehydrogenase
691	6909	10949	2.13	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 2S5S rRNA gene, isolate Tibet
1112	6118		19.14	1.3E+00	Y19213.1	NT	Homo sapiens putative psiliniba pseudogene for hair keratin, exons 2 to 7
1278	6277	11318	14.53	1.3E+00	4507989	NT	Homo sapiens zinc finger protein 157 (H2F22) (ZNF157) mRNA
1278	6277	11319	14.53	1.3E+00	4507990	NT	Homo sapiens zinc finger protein 157 (H2F22) (ZNF157) mRNA
1338	6336		1.06	1.3E+00	U61730.2	NT	Coli lacrma-jobi dihydrodipicolinate synthase (dapA) gene, complete cds
1574	6571		2.03	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 68 of the complete genome
2479	7448		1.67	1.3E+00	BE986735.2	EST_HUMAN	601661233/R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915545 3'
3517	8525	13538	0.68	1.3E+00	AF016404.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-prolylase enhancer protein (PCOLCE) genes, complete c>p
642	5870	10674	8.78	1.2E+00	AA676246.1	EST_HUMAN	2122d08.51 Scarec_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'
813	5834	10868	0.86	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE P(HRP-III))
813	5834	10869	0.86	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE P(HRP-III))
867	5885		1.83	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1143	6147	11179	6.07	1.2E+00	AF080245.2	NT	Elaeis oleifera sesquiterpene synthase mRNA, complete cds
1186	6187	11224	1.7	1.2E+00	AJ252242.1	NT	pea seed-bone mosaic virus complete genome

Page 5 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1188	6107	11225	1.7	1.2E+00	AJ256242.1	NT	pea seed-borne mosaic virus complete genome
1950	6946	12046	0.97	1.2E+00	AF146831.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3092	8108	13124	6.13	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3092	8108	13125	6.13	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3213	8228	3.28	1.2E+00	P54910	SWISSPROT	CONJUGATE TRANSFER PROTEIN PRECURSOR	
3277	8289	13314	0.73	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, Intron 2
3650	8636	13641	8.37	1.2E+00	UJ75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
3880	8881	13884	2.04	1.2E+00	BF313570.1	EST_HUMAN	MR0-FT0175-050900-203-908_1 FT0175 Homo sapiens cDNA
4174	8289	13314	0.97	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, Intron 2
4273	9268	14257	1.01	1.2E+00	6980951	NT	Rattus norvegicus Glycine receptor alpha 2 subunit (glycine receptor, neomethyl) (GIRr2), mRNA
4346	9337		2.1	1.2E+00	MB7060.1	NT	Rattus rattus cardiac A ₂ U gene, exons 1-23
4392	9383	14365	0.89	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4429	9419	14405	1.92	1.2E+00	AF168495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4456	9446		5.44	1.2E+00	Y09200.1	NT	T. pallidum chloroplast tbc1 gene, partial
461	5488	10509	1	1.1E+00	D86080.1	NT	Human mRNA for KIAA0227 gene, partial cds
1725	6720	11798	1.36	1.1E+00	AWB65393.1	EST_HUMAN	QVO-BN0042-170300-163-912 BH00421 Homo sapiens cDNA
3255	8268	13280	7.24	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3255	8269	13291	7.24	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3406	8415	13443	0.72	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3479	8487		2.43	1.1E+00	8922873	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
3499	8507	13522	0.93	1.1E+00	AI80860.1	EST_HUMAN	Wf54h11.x1 Scares_NFL_7_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SWIP531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ;
3636	8642	13647	1.32	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3636	8842	13648	1.32	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3840	8842	13649	0.95	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3913	8913	13908	0.88	1.1E+00	6756205	NT	Mus musculus proteasome (prosome, macropain) subunit, delta type 7 (Pamb7), mRNA
4094	8088		8.1	1.1E+00	5835331	NT	R. unicornis complete mitochondrial genome
4834	9818	14798	4.26	1.1E+00	U18468.1	NT	African swine fever virus, complete genome
4899	9878	14847	1.11	1.1E+00	X78425.1	NT	E. faecalis ppp5 gene
5024	8995	14868	0.71	1.1E+00	P25396	SWISSPROT	TELLURITE RESISTANCE PROTEIN TE1HA
5058	10028	14986	0.97	1.1E+00	AJ251695.1	NT	Mus musculus Kcnq1, Ltpc5, Mash2, Tsc4 and Tsc5 genes, alternative transcripts
98	5175		3.83	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
113	5185	10194	2.17	1.0E+00	DB8425.1	NT	Cavia cobaya mRNA for seminiferous tubule kinase, complete cds
415	5452		2.22	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 16S rRNA, 6S rRNA and 28S rRNA

Page 6 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.:	Top Hit Database Source	Top Hit Descriptor
671	5604	10802	1.67	1.0E+00	AJ251660.1	NT	Girardia ligata mRNA for homeodomain transcription factor (so gene)
669	5694	10703	9.1	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
670	5695		0.89	1.0E+00	AF25584.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1365	7746		3.02	1.0E+00	XK0416.1	NT	V. carteri Algal-CAM mRNA
1719	8714	11791	1.39	1.0E+00	AB008631.1	NT	Pleuropelvic stellate intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2414	7385	12564	1.05	1.0E+00	P48355	SWISSPROT	DNA GYrase SUBUNIT B
2414	7385	12505	1.05	1.0E+00	P48355	SWISSPROT	DNA GYrase SUBUNIT B
2806	7826	12841	3.99	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2806	7826	12842	3.99	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2897	7816		0.93	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN CBF12.08C IN CHROMOSOME 1
3126	8142	13163	0.82	1.0E+00	AA828453.1	EST_HUMAN	ai28608_s1 Sares_totoel_felis_Nb2Hf8_9rw Homo sapiens cDNA clone IMAGE:1032830 3' similar to
3519	5175		0.92	1.0E+00	U23808.1	NT	WP:CA2D8.3 CE0204 contains element MER22 MER22 repetitive element;
3597	8804	13812	1.71	1.0E+00	AJ223816.1	NT	Xenopus laevis rhodopsin gene, complete cds
3856	6954	13843	1	1.0E+00	AF22391.1	NT	Agaricus bisporus mRNA for tyrosinase
4153	9148		1.07	1.0E+00	8822245	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4660	9845	14633	1.73	1.0E+00	AL163247.2	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
4751	9736		1.35	1.0E+00	U75741.1	NT	Homo sapiens chromosome 21 segment HS21C047
4839	9840		0.93	1.0E+00	D10852.1	NT	Taenia ovis 45W antigen (Tow4) gene, complete cds
4978	8954		1.12	1.0E+00	AF200817.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
5031	10002		1.38	1.0E+00	AJ245481.2	NT	Pilot whale milt/fish phosphoprotein (P) gene, partial cds
2566	7529	12647	0.95	9.9E-01	AL163302.2	NT	Human immunodeficiency virus type 1 proviral complete genome, isolate 95M(LB4)
3524	8531		0.82	9.9E-01	AF174585.1	NT	Homo sapiens chromosome 21 segment HS21C102
519	5554	10557	0.97	9.8E-01	P22587	SWISSPROT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
2729	7686		0.98	9.8E-01	AF174644.1	NT	AMINO-ACID ACETYL TRANSFERASE (LACETYL GLUTAMATE SYNTHASE) (AGS) (NAGS)
4315	9307	14281	0.68	9.6E-01	AF197926.1	NT	Xenopus laevis lac CTPase mRNA, complete cds
4316	9307	14292	0.68	9.6E-01	AF197926.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (Pgm1) mRNA, complete cds
4336	9327	14312	1.34	9.6E-01	AW789874.1	EST_HUMAN	Bromus inermis putative cytosolic phosphoglucomutase (Pgm1) mRNA, complete cds
2404	7375	12495	1.44	9.5E-01	7705591	NT	PM2-UM0053-240300-005-f12 U10053 Homo sapiens cDNA
3694	8698	13869	2.08	9.6E-01	BE802340.1	EST_HUMAN	Xenopus laevis CG-125 protein (LOC51003), mRNA
							5011875659F11NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3855473 5'

Page 7 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3694	8698	13700		2.08	9.5E-01 BE02340.1	EST_HUMAN	601675639F-1 NIH_MGC_21 Homo sapiens cDNA clone [MAGE:39563473 5'
3128	8144			3.87	9.4E-01 AF165980.1	NT	Bartonella claridgeae RNA polymerase beta subunit (rpB) gene, partial cds
3146	8162			1.76	9.4E-01 AF080595.1	NT	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
6694	6689			1.02	9.3E-01 AF242382.1	NT	Homo sapiens phenylony-C6A hydroxylase (PHY1) gene, exon 5
2692	7526	12844		2.28	9.0E-01 BE01172.1	EST_HUMAN	RC3-B10503-271198-011-B01 BT0503 Homo sapiens cDNA clone [MAGE:3916184 3'
3166	8182	13205		3.17	9.2E-01 BE6322702.1	EST_HUMAN	601441338F-1 NIH_MGC_72 Homo sapiens cDNA clone [MAGE:3916184 3'
2065	7047			2.24	9.1E-01 8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3132	8148	13168	0.83	9.1E-01 T28418.1	EST_HUMAN	AB200GGR Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'	
3132	8148	13169	0.83	9.1E-01 T28418.1	EST_HUMAN	AB200GGR Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'	
4254	9248	14232	1.01	9.0E-01 AF09810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds	
4411	9401	14386	2.16	8.8E-01 O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE	
462	5499	10510	1.83	8.7E-01 AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds	
2804	7824	12839	5.88	8.7E-01 AA585893.1	EST_HUMAN	mn0511.s1 NCI_CGAP_P44.1 Homo sapiens cDNA clone [MAGE:1078877	
							Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzate 1,2-dioxigenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzate 1,2-dioxigenase alpha-ISP protein OhbB (ohbB), and putP
4847	9829		4	8.7E-01 AF121970.1	NT		
471	5507	163	8.6E-01 X17012.1	NT			
848	5867	10808	8.21	8.6E-01 W69089.1	EST_HUMAN	zd44fe03.1 Soares fetal heart_NbHH190V Homo sapiens cDNA clone [MAGE:343516 5'	
3539	8545	13552	0.72	8.6E-01 AL161585.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65	
3710	8714	13716	1.03	8.6E-01 U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds	
732	5755	10776	2.07	8.3E-01 M93437.1	NT	Thermus thermophilus cytochrome c-552 (cytA) and CytB (cytB) genes, complete cds	
3021	8039	13047	3.04	8.3E-01 AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18	
3805	8805	13803	2.61	8.3E-01 Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster	
1999	8982	12088	1.68	8.2E-01 AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds	
2608	7570		1.22	8.2E-01 AW379890.1	EST_HUMAN	IL3-CT219-161199-031-C08 C10219 Homo sapiens cDNA	
3819	8821	13828	0.93	8.2E-01 AF063417.1	NT	Tanysylum obliquum elongation factor 1-alpha mRNA, partial cds	
4935	8912	14890	0.89	8.2E-01 AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds	
2684	7612		0.93	8.1E-01 AF191939.1	NT	Mus musculus TANK binding kinase TBK1 (TBK1) mRNA, complete cds	
3376	8384	13404	2.84	8.1E-01 AF055086.1	NT	Homo sapiens MHC class 1 region	
3376	8384	13405	2.84	8.1E-01 AF055066.1	NT	Homo sapiens MHC class 1 region	
178	5240		2.17	8.0E-01 AJ271510.1	NT	Staphylococcus aureus partial pla gene for phosphate acetyltransferase allele 15	
286	5344	10356	8.83	8.0E-01 AJ13272.1	NT	Bos taurus fulb and rlf genes	

Page 8 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1984	6969			1.42	8.0E-01	BF330982.1	EST_HUMAN
3003	8021	13034		1.22	8.0E-01	AF27397.1	NT
3239	8232	13273		1.18	8.0E-01	AB008193.1	NT
3621	8628			1.19	8.0E-01	AL162758.2	NT
4402	9363	14377		7.03	8.0E-01	X837392.2	NT
4822	9806	14768		1.12	8.0E-01	7887332	NT
451	6488	10503		1.55	7.9E-01	D11476.1	NT
705	6729			0.79	7.9E-01	AE002130.1	NT
1568	6585			14.05	7.9E-01	AB040885.1	NT
2201	7179	12302		8.75	7.9E-01	AB004616.1	NT
2202	7180	12303		1.53	7.9E-01	AF130459.1	NT
3438	8446	13472		2.93	7.9E-01	AF228684.1	NT
4176	9170			0.79	7.9E-01	BE283612.1	EST_HUMAN
4479	9469	14449		1.35	7.9E-01	67531745	NT
4478	9469	14450		1.36	7.9E-01	67531745	NT
865	5883			2.29	7.9E-01	Z43785.1	EST_HUMAN
2213	7190	12311		2.82	7.8E-01	AW569567.1	EST_HUMAN
4563	8551	14537		0.79	7.8E-01	UB7305.1	NT
4871	9850			1.61	7.8E-01	AW733353.1	EST_HUMAN
143	5209	10223		4.43	7.7E-01	AF184345.1	NT
716	5739			1.61	7.7E-01	AF050157.1	NT
2640	7600	12714		1.66	7.7E-01	O33915	SWISSPROT
3520	8527	13538		3.71	7.7E-01	AF118085.1	NT
4272	9265	14255		3.89	7.7E-01	AF189488.1	NT
4272	9265	14256		3.89	7.7E-01	AF189488.1	NT
509	5544			1.38	7.5E-01	AL183301.2	NT
579	6811	10610		1	7.5E-01	AF020503.1	NT
6070	10039	16006		0.95	7.5E-01	6981387	NT
1113	6119	11147		1.25	7.4E-01	A1598146.1	EST_HUMAN

Page 9 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2281	7257	12376	0.97	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
3643	8849	13855	0.87	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
4184	9177	14161	8.61	7.4E-01	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21(C048
5013	9884	14860	1.07	7.4E-01	AW270842.1	EST_HUMAN	XP83d04_x1 NCI_CGAP_Ova0 Homo sapiens cDNA clone IMAGE:2740951 3' similar to contains element MER35 MER35 repetitive element
4483	9473	14453	0.84	7.3E-01	AE001166.1	NT	Bacillus burgdorferi (section 52 of 70) of the complete genome
4552	9850	14536	4.94	7.3E-01	AF228421.1	NT	Homo sapiens HT017 mRNA, complete cds
5046	10017	14986	0.92	7.3E-01	AJ400881.1	NT	Cicer arietinum partial mRNA for putative UDP-glycosc
821	5841		2.09	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
1917	6903	11987	3.43	7.2E-01	X79140.1	NT	N. fabaceum Nef-4A13 mRNA
2382	7363	12485	1.25	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin-2-receptor, complete cds
2883	8011	13023	1.4	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3370	8378	13388	2.78	7.2E-01	AF065608.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6/A-1 allele, complete cds
3533	8539	13545	0.98	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0369 gene, partial cds
3780	8783	13787	2.44	7.2E-01	BF338305.1	EST_HUMAN	SG2035589F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:41832225'
4624	8609	14587	3.41	7.2E-01	DB0314.1	NT	L-mesentericoids gene for sucrose phosphorylase (EC 2.4.1.7)
							Homo sapiens transcription factor (GHM) enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α 2
4849	8926	14904	1.37	7.2E-01	AF198779.1	NT	Homo sapiens transcription factor (GHM) enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α 2
4975	9951	14929	0.78	7.2E-01	P33066	SWISSPROT	NUCLEOSIDE TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE 1)(NPH 1)
683	5707	10719	9.06	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
2889	8007	13020	14.39	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4086	9080	14070	3.49	7.1E-01	7305360	NT	Mus musculus oligolin (Olig), mRNA
4086	8080	14071	3.49	7.1E-01	7305360	NT	Mus musculus oligolin (Olig), mRNA
1209	6209	11248	2.58	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1209	6209	11249	2.58	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2381	7353	12474	1.03	7.0E-01	NB2412.1	EST_HUMAN	Y73e07_51 Saccharomyces cerevisiae multiple scleriosis cDNA clone IMAGE:288708 3' similar to contains Alt repetitive element

Page 10 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2361	7353	12475	1.03	7.0E-01	N82412.1	EST_HUMAN	y773e07.31 Scores_7multiple_sclerosis_2NfHMSp Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
4889	6868		1.81	7.0E-01	AL16301.2	NT	Homo sapiens chromosome 21 segment HS21C101
955	5971	11004	15.83	6.8E-01	U69874.1	NT	<i>Candida albicans</i> squalene epoxidase (CERG1) gene, complete cds and translational regulator gene, partial cds
955	5971	11005	16.83	6.9E-01	U69874.1	NT	<i>Candida albicans</i> squalene epoxidase (CERG1) gene, complete cds and translational regulator gene, partial cds
1281	6280	11334	1.72	6.9E-01	AA563530.1	EST_HUMAN	mn28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3148	8164	13184	1.66	6.9E-01	AE002271.2	NT	<i>Chlamydia muridarum</i> , section 3 of 85 of the complete genome
942	5959	10992	2.14	6.8E-01	AF017764.1	NT	<i>Giardia intestinalis</i> carbamate kinase gene, complete cds
2603	7565		1.2	6.8E-01	D96917.1	NT	Synecytosis sp. PCC6803 complete genome, 27/27, 3418852-3573470
4439	6429	14413	1.39	6.8E-01	J00762.1	NT	Rat(hooded) plectin gene : exon III and flanks
286	5353	10366	24.4	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete cds
337	5389	10396	21.87	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete cds
2086	7087	12179	1.15	6.7E-01	AA451864.1	EST_HUMAN	zx12g12.31 Scores_total_fetus_Nb2HF8_3w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element;
2102	7763	12188	2.56	6.7E-01	AF186073.1	NT	Drosophila melanogaster Mat85C gene, complete cds; NM/DMC isoform (Nm85c) gene, complete cds, alternatively spliced; and transcription factor (Raf1ish) gene, complete cds, alternatively spliced
2827	7946	12863	4	6.7E-01	6678580	NT	<i>Mus musculus</i> Wiskott-Aldrich syndrome protein (Wasp), mRNA
4331	93222	14308	0.7	6.7E-01	X74421.1	NT	<i>S. tuberosum</i> mRNA for glucose-6-phosphate dehydrogenase
2828	7588	12700	1.28	6.6E-01	AF198939.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3409	8418	13446	0.83	6.6E-01	4506880	NT	Homo sapiens samsa domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMASA) mRNA
3574	8561	13587	3.48	6.6E-01	Y07669.1	NT	<i>C. albicans</i> s random DNA marker, 262bp
3993	8890						Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-I) gene, Ror1 gene, and sodium phosphate transporter (NPT3) gene, complete cds
618	6845	10847					<i>H. vulgaris</i> Na,K-ATPase alpha subunit mRNA, complete cds
618	6845	10848					<i>H. vulgaris</i> Na,K-ATPase alpha subunit mRNA, complete cds
3348	8357	13315					<i>Mus musculus</i> gene for Tob2, complete cds
4159	9154	14337	6.18	6.5E-01	AJ272285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8

Page 11 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4994	9873	14840		2.32	6.5E-01	U28921.1	NT
5073	10042	15008		1.39	6.6E-01	8924057	NT
250	5310	10321		8.85	6.4E-01	U48848.1	NT
2511	7479	12594		0.9	6.4E-01	AF161164.1	NT
3374	8382	13402		3.74	6.4E-01	U48854.2	NT
3771	8774	13778		1.19	6.4E-01	AB046827.1	NT
4264	9355	14334		0.74	6.4E-01	Y12488.1	NT
4364	9355	14335		0.74	6.4E-01	Y12488.1	NT
431	5469	10488		3.16	6.3E-01	P05228	SWISSPROT
631	5568	10569		1.73	6.3E-01	U32689.1	NT
2098	7078	12193		26.01	6.3E-01	U81136.1	NT
2503	7471	12587		1.82	6.3E-01	U75331.1	NT
2503	7471	12588		1.82	6.3E-01	U75331.1	NT
2849	7988			0.67	6.3E-01	Y17276.1	NT
2330	7304			3.53	6.1E-01	6678076	NT
4405	9396	14379		0.98	6.1E-01	4557538	NT
491	5527	10535		1.08	6.0E-01	DB7675.1	NT
557	5591			2.78	6.0E-01	6802999	NT
1345	6342	11393		1.38	6.0E-01	AF065283.1	NT
3725	8729	13727		0.81	6.0E-01	AJ233396.1	NT
3923	8923	13914		2.18	6.0E-01	X16842.1	NT
4084	9058			1.03	6.0E-01	AF058895.1	NT
985	6000	11034		1.03	5.9E-01	U32701.1	NT
3196	8212	13233		9.18	5.9E-01	AL163267.2	NT
3186	8212	13234		9.18	5.9E-01	AL163267.2	NT
4100	9094			3	5.9E-01	AF162756.1	NT
1866	6885	11943		1.05	5.8E-01	P40472	SWISSPROT
3876	8877	13880		0.87	5.8E-01	BF695738.1	EST_HUMAN
4383	9374	14353		4.1	5.8E-01	AB080977.1	NT
4652	9837			1.31	5.8E-01	AF110846.1	NT
4775	9759			2.29	5.8E-01	AW789483.1	EST_HUMAN
1483	8460	11518		1.04	6.7E-01	P08727	SWISSPROT
1463	6460	11519		1.04	6.7E-01	P08727	SWISSPROT

Page 12 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3162	8168	13188	1.38	5.7E-01	Q8WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A)
3425	8433		2.37	6.7E-01	AB033503.1	NT	Populus tremuloides peacs-2 mRNA for 1-aminocyclopentane-1-carboxylate synthase, complete cds
5042	10013	14982	0.95	5.7E-01	L41887.1	NT	Drosophila extra sex comb gene, exon 1-4, complete cds
3283	6285	13320	1.11	5.6E-01	AB018238.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3283	8285	13321	1.11	5.6E-01	AB018233.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
4117	9111	14095	2.28	6.6E-01	D83135.1	NT	Chicken TBP gene, exon 8, complete cds
1182	6183	11230	1.79	5.5E-01	8393912	NT	Rattus norvegicus Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2629	7589	12701	2.21	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2829	7589	12702	2.21	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2848	7889	12884	0.79	5.5E-01	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog) like (SKIV2L), mRNA
2892	8010			1.33	5.5E-01	H46218.1	EST_HUMAN
3163	8178	13201	3.6	5.6E-01	AF227240.1	NT	Y01810.81 Soares adult brain N2b5-HB56Y Homo sapiens cDNA clone IMAGE:1782683
3608	8615	13624	1.37	5.6E-01	P48765	SWISSPROT	Rabbit oral papillomavirus, complete genome
4982	9987	14935	0.89	5.5E-01	U68097.1	NT	FOS-RELATED ANTIGEN-1
144	5210	10224	13.68	5.4E-01	7857268	NT	Bos taurus MHC class II beta ₂ -chain B ₂ A-D ₁ B ₁ gene, partial cds
144	5210	10225	13.68	5.4E-01	7857268	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
580	5812	10811	1.77	5.4E-01	AF232006.1	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
580	5812	10812	1.77	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gata (gta) genes, complete cds, and unknown genes
580	6280	11281	2.4	5.4E-01	AW886087.1	EST_HUMAN	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gata (gta) genes, complete cds, and unknown genes
2048	7030		2.35	6.4E-01	AE002247.2	NT	QV4-NN0040-07040-160-c04 NN0040 Homo sapiens cDNA
2193	7172	12283	1.53	6.4E-01	AJ276882.1	NT	Chlamydomonas reinhardtii AR39, section 74 of 94 of the complete genome
612	5547	10552	1.61	5.3E-01	AF019413.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
2710	7667	12779	10.07	5.3E-01	4506328	NT	Homo sapiens class II region containing tenascin X (tenascin-X) gene, partial cds, cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
2710	7667	12780	10.07	6.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3163	8185	13206	3.67	5.3E-01	AF087653.1	NT	Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds

Page 13 of 209
 Table 4
 Single Exon Probes Expressed In HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4080	8084			1.22	5.3E-01 U39887.1	NT	<i>Mycoplasma genitalium</i> section 9 of 51 of the complete genome
808	5827	10857		12.62	5.2E-01 L20770.1	NT	<i>Drosophila melanogaster</i> helix-loop-helix mRNA, complete cds
1146	6150	11182		11.32	5.2E-01 Q8WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NFAT5) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1171	6174	11208		8.03	5.2E-01 AF224492.1	NT	<i>Homo sapiens</i> phospholipid scramblase 1 gene, complete cds
1847	85356			4.17	6.2E-01 AL163285.2	NT	<i>Homo sapiens</i> chromosome 21 segment HS21C0085
2085	7086	12178		1.52	6.2E-01 AB016283.2	NT	<i>Homo sapiens</i> mRNA for KIAA0740 protein, partial cds
3046	8083	13071		1.72	5.2E-01 U65942.1	NT	<i>Chlamydophila abortus</i> strain SP81 POMP91A and POMP80A precursor, genes, complete cds
3321	8331			11.56	5.2E-01 AL116780.1	NT	<i>Bacillus cereus</i> strain T4 cDNA library under conditions of nitrogen deprivation
3360	8368	13387		2.52	5.2E-01 AA0884165.1	EST HUMAN	am77g05.s1 Strategene Schizo brain S11 Homo sapiens cDNA clone IMAGE:6165043
3547	8554			0.79	5.2E-01 AF020268.1	NT	<i>Medicago sativa</i> chloroplast 1 malate dehydrogenase precursor (p1 mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
4368	8349			1.48	6.2E-01 AF093786.1	NT	<i>Avian Infectious bronchitis virus</i> Isolate variant 2 S1 spike glycoprotein gene, partial cds
4980	8937			1.01	5.2E-01 AL163281.2	NT	<i>Homo sapiens</i> chromosome 21 segment HS21C081
613	5640	10843		1.9	5.1E-01 M58569.1	NT	<i>Human adrenodoxin reductase</i> gene, exons 3 to 12
640	58688	10871		3.68	5.1E-01 AJ233944.1	NT	<i>Polyangium vitellinum</i> (strain PI vtl) 16S rRNA gene
640	58688	10872		3.68	5.1E-01 AJ233944.1	NT	<i>Polyangium vitellinum</i> (strain PI vtl) 16S rRNA gene
3963	8981	13951		4.37	5.1E-01 AJ858495.1	EST HUMAN	wi39612.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2427263 3'
4062	9058	14043		2.47	5.1E-01 P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
2076	7058	12167		1.03	5.0E-01 4885552	NT	<i>Homo sapiens</i> postmeiotic segregation increased 2-like 9 (PMS2L9) mRNA
2076	7058	12168		1.03	5.0E-01 4885552	NT	<i>Homo sapiens</i> postmeiotic segregation increased 2-like 9 (PMS2L9) mRNA
2083	7084	12174		1.08	5.0E-01 AF0008210.1	NT	<i>Buchnera aphidicola</i> genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaE), ATP operon (lapCDGAHFEB), and putative chromosome replication protein (gldA) genes, complete cds; and termination factor Rho (rho) gene>
2083	7064	12175		1.08	5.0E-01 AF0008210.1	NT	<i>Buchnera aphidicola</i> genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaE), ATP operon (lapCDGAHFEB), and putative chromosome replication protein (gldA) genes, complete cds; and termination factor Rho (rho) gene>
3740	8744	13744		1.11	5.0E-01 L38483.1	NT	<i>Rattus norvegicus</i> lagged protein mRNA, complete cds
3782	8785	13788		2.97	5.0E-01 AB035301.1	NT	<i>Homo sapiens</i> mRNA for KIAA1184 protein, partial cds
781	6802	10832		2.67	4.9E-01 BF571462.1	EST HUMAN	652076619F1_NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4249860 5'
1619	6816	11682		4.83	4.9E-01 AJ243985.1	NT	<i>Xenopus laevis</i> mRNA for c-jun protein, 1978 BP
1864	6853	11941		1.9	4.9E-01 U40869.1	NT	<i>Cavia porcellus</i> pulmonary surfactant protein A (SP-a) mRNA, complete cds
3460	8468			1.14	4.8E-01 AA912842.1	EST HUMAN	3d92ad8.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:16251443'
3658	8664	13069		1.62	4.6E-01 BF663300.1	EST HUMAN	602081103F1_NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4215481 6'

Page 14 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3658	8664	13670	1.62	4.6E-01	BF093300.1	EST_HUMAN	602081103F1_NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4265481 5'
2789	7819	12838	4.48	4.5E-01	AA677086.1	EST_HUMAN	256d02_s1 Scores: fetal liver, spleen, 1NF1S_S1 Homo sapiens cDNA clone IMAGE:464178 3'
3243	8256	13277	4.25	4.5E-01	Q05783	SWISSPROT	BASEMENT PRECURSOR (HSPG) (PERLECAN) (PLC)
3283	8304	13329	1.39	4.5E-01	AF128318.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
3917	8917		1.06	4.5E-01	Q28247	SWISSPROT	COLLAGEN ALPHA 3(V) CHAIN
4052	10058		5.38	4.5E-01	AW872485.1	EST_HUMAN	h609g02_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
4786	9770	14754	1.55	4.5E-01	BE863445.2	EST_HUMAN	601867225F1_NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
1885	6970		2.19	4.4E-01	6680503	NT	Mus musculus Integral membrane-associated protein 1 (Itmip1), mRNA
2325	7289	12420	4.73	4.4E-01	P48765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3241	8254	13275	1.18	4.4E-01	AF058780.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3241	8254	13276	1.18	4.4E-01	AF058780.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3245	9258	13278	1.81	4.4E-01	BF056726.1	EST_HUMAN	7B1d02_y1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:33B3795 5'
4113	9107		1.55	4.4E-01	BE378707.1	EST_HUMAN	601237138F1_NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5'
4838	9815	14894	6.65	4.4E-01	U61164.1	NT	Buzura suppressaria nucleopolyhedrovirus ecdysteroid UDP-glucosyltransferase (egf) gene, complete cds
408	5145	10485	1.95	4.3E-01	AF165218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
408	5445	10486	1.85	4.3E-01	AF165218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
2801	7821		1.34	4.3E-01	AW895289.1	EST_HUMAN	CM2-DT0003-010200-077-001 DT0003 Homo sapiens cDNA
2886	8004	13016	0.72	4.3E-01	AW899477.1	EST_HUMAN	MRO-BN0070-270300-008-804 BN0070 Homo sapiens cDNA
4028	9024	14011	1.2	4.3E-01	J00306.1	NT	Human somatostatin 1 gene and flanks
4282	5145	10485	1.07	4.3E-01	AF165218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4282	5445	10486	1.07	4.3E-01	AF165218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4944	9821		1.08	4.3E-01	B035250	NT	Xestia c-nigrum granulatus, complete genome
1341	7745	11389	1.24	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FITSH HOMOLOG PRECURSOR
3528	8534	13541	3.83	4.2E-01	AE003947.1	NT	Xylella fastidiosa, section 83 of 229 of the complete genome
3552	8559	13565	2.9	4.2E-01	AI280338.1	EST_HUMAN	Q84d01_x1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1870945 3'
3629	10057		0.86	4.2E-01	NB1203.1	EST_HUMAN	7881E1 fetal brain cDNA Homo sapiens cDNA clone IMAGE:7881E1_K similar to R07879_Z40488
4558	8546	14531	5.45	4.2E-01	AA6534093.1	EST_HUMAN	Q89n01_s1 NC1 CGAP_P10 Homo sapiens cDNA clone IMAGE:987777 similar to g8-M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4836	9821	14613	3.8	4.2E-01	R13467.1	EST_HUMAN	J077601_x1 Scores: infant brain NIB Homo sapiens cDNA clone IMAGE:28278 6'
1077	6084	11113	1.62	4.1E-01	AB03481.1	EST_HUMAN	RC-BT091-210188-42 BT091 Homo sapiens cDNA
1086	6083	11122	2.08	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'

PCT/US 01/00661

Page 15 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1086	6093	11123	2.09	4.1E-01	AV705243.1	EST HUMAN	AV705243 ADB Homo sapiens cDNA clone ADDBAHF08 5'
1673	6570	11632	0.94	4.1E-01	AI805949.1	EST HUMAN	PM-BT103-270498-684_B1103 Homo sapiens cDNA
2638	7598	12712	1.1	4.1E-01	7705283.1	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2869	7888	12908	2.49	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2869	7888	12909	2.49	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3229	6244	13266	0.7	4.1E-01	AA908344.1	EST HUMAN	094-b08_s1 Soar es_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
4152	9147	14131	2.75	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 IsoG, IsoH, IsoI, IsoA, IsoB, IsoC, IsoD, IsoE and IsoF genes
4178	9172		0.74	4.1E-01	AA809257.1	EST HUMAN	om633d02_s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4532	6522	14509	1.37	4.1E-01	AV747880.1	EST HUMAN	AV747880 NPC Homo sapiens cDNA clone NP/CBDF10 5'
1022	6031	11061	0.81	4.0E-01	8404856	NT	Lequeus rubellus milchondria, complete genome
1319	6317	11365	1.16	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dml) mRNA, complete cds
1464	6451		3.09	4.0E-01	68792568	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfb), mRNA
2733	5207	10222	2.12	4.0E-01	6878490	NT	Mus musculus ubiquitin-protein ligase e3 component n-recognin (Ubr1), mRNA
2698	7817	12937	1.16	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2898	7817	12938	1.16	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3612	8810	13629	2.74	4.0E-01	AF068903.1	NT	Streptococcus pneumoniae YIC (yic), YID (yid), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3737	8741	13740	3.44	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3737	8741	13741	3.44	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4672	9857		8.8	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOCQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
1359	6356	11407	1.57	3.9E-01	AF208618.1	NT	Gorilla gorilla carboxy-ester lipase (CEL) gene, complete cds
2571	7534	12651	2.87	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2633	7593	12705	2.93	3.9E-01	X82032.1	NT	H.sapiens B-myb gene
2633	7593	12706	2.98	3.9E-01	X82032.1	NT	H.sapiens B-myb gene
3023	8040	13049	4.17	3.9E-01	AJ225896.1	EST HUMAN	Sinorhizobium meliloti egi, cya3 genes and ori3
3984	8982	13852	1.38	3.9E-01	BF592811.1	EST HUMAN	761d01_x1_NCL_CGAP_B118 Homo sapiens cDNA clone IMAGE:3339169 3'
159	6225		2.48	3.8E-01	7019488	NT	Homo sapiens protein kinase PRK1beta (p46beta), mRNA
502	5537		3.87	3.8E-01	AB026291.1	NT	Mus musculus cmr-1 mRNA for pericentriolar material-1, complete cds
2496	7484	12579	3.42	3.8E-01	AJ214117.1	NT	Arabidopsis thaliana putative c-myb-like transcription factor (MYB3R-3) mRNA, complete cds
2560	7775	12841	3.09	3.8E-01	6678002	NT	Mus musculus solute carrier family 1, member 6 (Slc16), mRNA
2933	7952		0.92	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE/MP1213)
2974	7982	13007	2.37	3.8E-01	AF043383.1	NT	Pleurocytes americanus amorphopilidase N (ampN) gene, partial cds
3403	8412	13438	8.3	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30

PCT/US 01/00661

Table 4
Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3461	8469			0.77	A1807210.1	EST_HUMAN	Wf38b12_x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3671	8876	13678	0.83	3.8E-01	BE154080.1	EST_HUMAN	PM0-H10338-200400-010-010-010_H10338_Homo sapiens cDNA
2410	7381	12499	6.9	3.7E-01	AB037851.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3378	8386	13407	10.03	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenic protein 4 precursor (BMP4) gene, complete cds
3779	8782	13798	1.12	3.7E-01	AA519482.1	EST_HUMAN	EST21715_Adrenal gland tumor Homo sapiens cDNA 5' end
4108	9102	14089	7.57	3.7E-01	A1218707.1	EST_HUMAN	Ok38c07_x1 Soares, NSF_F8_9W_OT_PA_P_S11 Homo sapiens cDNA clone IMAGE:1510188 3'
4193	9186	14187	1.65	3.7E-01	AW878037.1	EST_HUMAN	MR3-O70007-4880360-104-b02 OT0007 Homo sapiens cDNA
4285	9258	14248	3.38	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome
980	5985		8.28	3.8E-01	UB9241.1	NT	Human mmpb gene, partial cds
1285	6283	11339	2.38	3.8E-01	T80255.1	EST_HUMAN	yd34e05_r1 Soares, infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1285	6283	11340	2.38	3.8E-01	T80255.1	EST_HUMAN	yd34e05_r1 Soares, infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1872	6881	11949	3.81	3.8E-01	AW590184.1	EST_HUMAN	1933f02_x1 NCL_GCAP_GCG_Homo sapiens cDNA clone IMAGE:2847419 3'
1872	6881	11950	3.81	3.8E-01	AW590184.1	EST_HUMAN	1933f02_x1 NCL_CGAP_GCG_Homo sapiens cDNA clone IMAGE:2847419 3'
1912	6898	11953	4.8	3.8E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2208	7195		0.97	3.8E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2326	7300		2.62	3.8E-01	X76725.1	NT	P_irregular (P3804) gene for actin
2417	7388	12508	0.85	3.8E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-907 ST0171 Homo sapiens cDNA
2558	7523	12638	1.1	3.8E-01	P24208	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2828	10035		7.88	3.8E-01	AF1689485.1	NT	Drosophila melanogaster sugar transporter 3 (sug3) mRNA, complete cds
3388	8398	13420	1.83	3.8E-01	X78758.1	NT	H_sapiens serotonin transporter gene, exons 9 and 10
3388	8398	13421	1.83	3.8E-01	X78758.1	NT	H_sapiens serotonin transporter gene, exons 9 and 10
4284	9226		0.88	3.8E-01	BE1707883.1	EST_HUMAN	RC1-H10545-160600-014-812 HT0545_Homo sapiens cDNA
4610	8598	14652	1.49	3.8E-01	Y1526.1	NT	Z_mays mRNA for casein kinase II alpha subunit
4849	9891	14808	2.78	3.8E-01	AW359393.1	EST_HUMAN	1a02g01_x1 NCL_GCAP_Lu24_Homo sapiens cDNA clone IMAGE:2872568 3'
5037	10008	14978	1.26	3.8E-01	AE001187.1	NT	Treponema pallidum section 3 of 87 of the complete genome
1115	5187	10186	0.85	3.8E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
209	5223	10235	2.22	3.8E-01	6678933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
715	5738	10755	1.11	3.8E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51308), mRNA
715	5738	10756	1.11	3.8E-01	7706138	NT	Homo sapiens GAP-like protein (LOC51308), mRNA
771	5783	10821	2.75	3.8E-01	BF129786.1	EST_HUMAN	601811080R1_NIH_MGC_48_Homo sapiens cDNA clone IMAGE:4053651 3'
1580	6577	11841	0.92	3.8E-01	BF510688.1	EST_HUMAN	8018846532_NIH_MGC_18_Homo sapiens cDNA clone IMAGE:4124244 6'

Page 17 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1600	6598	11657	2	3.5E-01	U257778.1	NT	Reittus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2219	7198	12318	1.43	3.5E-01	PG6798	SWISSPROT	HOMEBOX PROTEIN HOXA4 (HOX-14) (MH-3)
2531	7774	12616	1.81	3.5E-01	AA223452.1	EST_HUMAN	Z08409.s1 Strategene NT2 neuronal precursor 83/230 Homo sapiens cDNA clone IMAGE:890872'3'
3717	8721		1.97	3.5E-01	AA84238.1	EST_HUMAN	inf603.s1 NCI_CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357'3'
4140	9135	14118	2.08	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hoxb5b) gene, complete cds
4777	9781	14748	6.2	3.5E-01	MT18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
697	5721		1.44	3.4E-01	A1242958.1	NT	Homo sapiens partial N-myb (exon 3), HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
881	6976	11010	5.81	3.4E-01	Y09768.2	NT	Pseudomonas fluorescens colR, colS genes, ori222 and partial insA gene
1306	6304	11391	1.78	3.4E-01	Y006564.1	NT	Autobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2338	7312	12433	1.66	3.4E-01	DD09081.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
2932	7981	12868	0.8	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2932	7851	12969	0.8	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3078	8092	13108	1.04	3.4E-01	DD90805.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3088	8104	13118	7.39	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3268	8281	13303	1.07	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3453	8461	13488	4.38	3.4E-01	AF106835.1	NT	Methylotonus sp. strain SS1 putative GtpE (grpE), DnaK (dnak), and putative DnaJ (dnaj) genes, complete cds
3701	8705		2.49	3.4E-01	BF449010.1	EST_HUMAN	7n94a1.x1 NCI_CGAP_Ovir8 Homo sapiens cDNA clone IMAGE:3572232'3' similar to TR:Q9UJ16
3839	8937		1.48	3.4E-01	AA58498.1	EST_HUMAN	7n94a10.x1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347'3'
4509	9498	14478	1.77	3.4E-01	BE0698912.1	EST_HUMAN	MR4-BT0403-230200-202-001 BT0403 Homo sapiens cDNA
4794	9778		4.55	3.4E-01	AI240973.1	EST_HUMAN	q95c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1887208'3' similar to contains Alu repetitive element,
14	6094	10078	16.57	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
108	5094	10078	4.08	3.3E-01	X07886.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
445	5492	10560	0.92	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
627	6695	10860	1.67	3.3E-01	7882485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1181	6183	11221	4.2	3.3E-01	Q12448	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1288	6287	11331	3.14	3.3E-01	BF68880.1	EST_HUMAN	60216401671 NIH_3T3 cells cDNA clone IMAGE:4300281'3'
1569	6568	11628	1.18	3.3E-01	8753655	NT	Mus musculus disintegrin 5 (Digr5), mRNA

Page 18 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1700 6695			2.03	3.3E-01	AA3322734.1	EST_HUMAN	EST36722 Embryo, 8 week Homo sapiens cDNA 5' end
1978 6983			1.4	3.3E-01	AF031148.1	NT	Methylococcus capsulatus strain Bath outer membrane protein MapB (mapB) gene, complete cds
2340 7314			2.72	3.3E-01	4507834.1	NT	Homo sapiens uridine monophosphate synthetase (uridylate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS) mRNA
2879 7893	12921		1.79	3.3E-01	AJ251805.1	NT	Bacteriophage phi-YeO3-12 complete genome
2947 7866			0.67	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 kD SUBUNIT) (CLMF P35)
2881 7989	13012		1.05	3.3E-01	AJ007832.2	NT	Streptomyces argillaceus mitomycin biosynthetic genes
3415 8424	13452		1.05	3.3E-01	AB02822.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3720 8724	13724		1.91	3.3E-01	OB4645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3727 8731	13729		1.01	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN (P1); PROTEIN P3)
3858 8860	13888		1.38	3.3E-01	AL161488.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3895 8895	13888		1.71	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase genes, partial cds
4186 9181			2.36	3.3E-01	4759025	NT	Homo sapiens RAS protein activator like 1 (GAP1 like) (RASAL1) mRNA
4242 9236			1.68	3.3E-01	D31682.1	NT	Rattus norvegicus DNA for reucalcin, partial cds
4551 9539			1.7	3.3E-01	AI539114.1	EST_HUMAN	Op78b12-x1 NCI CGAP_U3 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57622 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN)
4680 9876	14658		1.36	3.3E-01	D64003.1	NT	Synochrocytis sp. PCC6803 complete genome, 22/27, 27/55/03-28887886
5071 10040	15007		0.98	3.3E-01	AI021692.1	EST_HUMAN	10x04g09_x1 Seares_fetal_liver_spleen_1NF1L_S1 Homo sapiens cDNA clone IMAGE:1655392 3' similar to contains element MER4 repetitive element ;
494 6491			1.61	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
708 5732			0.78	3.2E-01	AI161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1144 6148	11180		10.13	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1233 6261	11304		2.24	3.2E-01	Z50202.1	NT	P. vulgaris arc5-1 gene
1367 6384	11413		6.08	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE TRANSPORT PROTEIN)
1737 6732	11809		1.1	3.2E-01	Z36041.1	NT	S cerevisiae chromosome II reading frame ORF YBR172c
1748 6741			4.36	3.2E-01	AW957194.1	EST_HUMAN	EST369284 MAGE resequences, MAGD_Homo sapiens cDNA
1748 6741			4.36	3.2E-01	AW957194.1	EST_HUMAN	EST369284 MAGE resequences, MAGD_Homo sapiens cDNA
2096 7077	12181		1.78	3.2E-01	BF203817.1	EST_HUMAN	601868804F1_NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111612 5'
2470 7438			2.58	3.2E-01	7710079	NT	Mus musculus Prokna1 homeobox (Pknx1), mRNA
2837 7597	12711		1.11	3.2E-01	AF060568.1	NT	Homo sapiens promyelocytic leukaemia zinc finger protein (PLZF) gene, complete cds
3045 8082	13070		1.07	3.2E-01	BF380745.1	EST_HUMAN	IL2-UT0073-180990-161-H11 UT0073 Homo sapiens cDNA

Page 19 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4270	9283	14253	1.73	3.2E-01	M18818.1	NT	
4369	9362	14342	1.43	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4587	9385		7.8	3.2E-01	BF683617.1	EST_HUMAN	602081972F1 NIH_ MGCI_81 Homo sapiens cDNA clone IMAGE:4246305 5'
5054	10025	14984	1.02	3.2E-01	AL161514.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 26
2600	7562	12680	2.32	3.1E-01	R18051.1	EST_HUMAN	yes0n06_r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:MB6241 QM PROTEIN (HUMAN);
2625	7708	12696	2.72	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2625	7709	12697	2.72	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2785	7806		1.27	3.1E-01	AW828036.1	EST_HUMAN	h146h08_x1 Scores NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:2976391 3'
3100	8116		3.43	3.1E-01	AB028069.1	NT	Mus musculus gene for Ser/Thr kinase KIAMRE, exon 6
3811	8814	13820	0.89	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
4803	9780	14770	5.69	3.1E-01	AED03684.1	NT	Xylella fastidiosa, section 130 of 228 of the complete genome
71	7889	10158	1.59	3.0E-01	87550083	NT	Mus musculus protein kinase C, epsilon (Pkcε), mRNA
252	6312	10323	9.02	3.0E-01	AJ271735.1	NT	Homo sapiens Xa pseudoeukaryotic region; segment 1/2
1204	6205	11242	1.65	3.0E-01	AW300400.1	EST_HUMAN	xs63f08_x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1478	6475	11532	3.47	3.0E-01	AJ006755.1	NT	Baibenopliera physalus genes encoding atrial natriuretic peptide
1760	6752	11837	1.03	3.0E-01	X98092.1	NT	A.Immersus putative gene encoding integrase, Mars2 (RP)
3139	8165		4.06	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alpG gene for polyglutamate hydrolase, complete cds
3774	8777	13781	1.81	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-28119B-001-001 ST0262 Homo sapiens cDNA
3867	8868	13871	0.98	3.0E-01	AJ271736.1	NT	Hom sapiens Xa pseudoeukaryotic region; segment 2/2
4382	9373	14352	2.28	3.0E-01	AJ006755.1	NT	Baibenopliera physalus gene encoding atrial natriuretic peptide
4589	9577		0.99	3.0E-01	AF167835.1	NT	Bacteriophage APESE-1, complete genome
1973	6898	12063	1.16	2.9E-01	AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
3110	8126	13146	1.04	2.9E-01	AF078111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds
3178	8184	13216	2.82	2.9E-01	AW764239.1	EST_HUMAN	PM1-C70328-171289-001-f12 CT0328 Homo sapiens cDNA
3178	8184	13217	2.82	2.9E-01	AW754239.1	EST_HUMAN	PM1-C70328-171289-001-f12 CT0328 Homo sapiens cDNA
3801	8804	13809	0.7	2.9E-01	AI610836.1	EST_HUMAN	Ip21a11_x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A
3959	8957	13946	12.27	2.9E-01	AB016426.1	NT	ZINC FINGER PROTEIN (HUMAN),contains element L1 repetitive element;
4359	9350	14329	1.05	2.9E-01	AA284468.1	EST_HUMAN	Cavia porcellus mRNA for glutathione s-transferase, complete cds
4545	9534		0.85	2.9E-01	AI63207.2	NT	2s7d12_r1 NCI CGAP_GC81 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains AU repetitive element;
							Homo sapiens chromosome 21 segment HS21C007

Page 20 of 208

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4946	8923			1.33	2.8E-01 AI670699.1	EST_HUMAN	wa0603_x1_NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297309 3' similar to contains L1.12 L1 repetitive element;
5020	8991			1.01	2.8E-01 AL161665.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 81
563	6597			2.11	2.8E-01 U67713.6.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP160 mRNA, complete cds
698	5801			0.7	2.8E-01 L28145.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1087	6076	11108		2.54	2.8E-01 AF168050.1	NT	Guita guita oocyte maturation factor Mos (C-mos) gene, partial cds
1258	6256	11289		0.98	2.8E-01 BE313442.1	EST_HUMAN	601148733F1 NIH MGIC 19 Homo sapiens cDNA clone IMAGE:3163688 5'
1258	6256	11289		0.98	2.8E-01 BE313442.1	EST_HUMAN	601148733F1 NIH MGIC 19 Homo sapiens cDNA clone IMAGE:3163688 5'
1272	6270	11310		0.92	2.8E-01 D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1689	6685	11761		2.03	2.8E-01 AW860020.1	EST_HUMAN	QY1-C70384-120200-085-505 CT0364 Homo sapiens cDNA
1862	6948	12050		1.44	2.8E-01 AL047920.1	EST_HUMAN	DKFZp58B12321_1/1 688 (synonym: hule1) Homo sapiens cDNA clone DKFZp58B12321
2073	7055	121685		1	2.8E-01 AW51195.1	EST_HUMAN	hd44b03_x1 Soares cDNA clone IMAGE:2912333 3'
2401	7372	12493		2.06	2.8E-01 AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2401	7372	12494		2.06	2.8E-01 AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2476	7445			1.49	2.8E-01 AL161955.2	NT	Arabidopsis thaliana chromosome 4, contig fragment No. 65
2594	7557	12871		1.4	2.8E-01 AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2801	7820			1.35	2.8E-01 AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (TSP90) mRNA, partial cds
2802	7921	12941		2.3	2.8E-01 Z14037.1	NT	B.taurus microsatellite (ET1H121)
2802	7921	12942		2.3	2.8E-01 Z14037.1	NT	B.taurus microsatellite (ET1H121)
3294	8305	13330		0.85	2.8E-01 AP00004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 77/001-99/000 nt. position (4/7)
3890	8890	13898		1.44	2.8E-01 AE001180.1	NT	Borrelia burgdorferi (section 68 of 70) of the complete genome
4005	8001			0.91	2.8E-01 AE004450.1	NT	Pseudomonas aeruginosa PA01, section 11 of 529 of the complete genome
4075	8009			2.38	2.8E-01 AI09088.1	EST_HUMAN	ov49g10_x1 Soares testis_NHt Homo sapiens cDNA clone IMAGE:1640228 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
4337	8328	14313		2.15	2.8E-01 P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4682	8687	14649		2.85	2.8E-01 AF030154.1	NT	Bovine adenovirus 3 complete genome
4711	8686	14680		1.28	2.8E-01 BF528188.1	EST_HUMAN	602042601F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180129 5'
4731	8716	14701		2.3	2.8E-01 AI272697.1	EST_HUMAN	q559e11_x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element;
6004	8975	14850		1.68	2.8E-01 AA767084.1	EST_HUMAN	ca41f01_s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1307668 3'
473	6509	10522		2.82	2.8E-01 Y17324.1	NT	Rattus norvegicus CDK104 mRNA
609	5636	10637		2.19	2.7E-01 AA450061.1	EST_HUMAN	2x30b10_s1 Soares_total_fetus_Nb2h1F8_Ew Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element;
1242	6240	11281		1.87	2.7E-01 AB004906.1	NT	[pcomesa purpurea transposable element Tp100 gene for transposase, complete cds

Page 21 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1682	6579			1.3	2.7E-01	X7815.1	NT
1691	6887	11762		2.21	2.7E-01	W58087.1	EST_HUMAN
1739	6734	11811		1.16	2.7E-01	P03341	SWISSPROT
2077	7762			1.42	2.7E-01	AF047375.1	NT
2306	7281	12398		6.34	2.7E-01	Y13886.1	NT
2386	7367	12479		2.78	2.7E-01	AI310858.1	EST_HUMAN
2915	7834			0.72	2.7E-01	BFO8284.1	EST_HUMAN
3804	8904	13802		1.88	2.7E-01	AI928015.1	EST_HUMAN
3918	8918	13911		2.28	2.7E-01	L77569.1	NT
4739	9724	14709		1.14	2.7E-01	L27516.1	NT
4875	9854			4.26	2.7E-01	AW556131.1	EST_HUMAN
487	7721	10516		1.71	2.6E-01	P78411	SWISSPROT
477	6514			1.09	2.6E-01	D16459.1	NT
1370	6367	11416		1.36	2.6E-01	BE885087.1	EST_HUMAN
1410	6408	11466		0.82	2.6E-01	AB013280.1	NT
1856	6845	11932		4.92	2.6E-01	AL161472.2	NT
1856	6845	11933		4.92	2.6E-01	AL161472.2	NT
2037	7020			7	2.6E-01	AW733152.1	EST_HUMAN
2062	7073	12187		1.04	2.6E-01	M11844.1	NT
2402	7373			3.6	2.6E-01	Y12896.1	NT
2475	7444			5.05	2.6E-01	BE272440.1	EST_HUMAN
3018	8035			1.09	2.6E-01	AW874531.1	EST_HUMAN
3558	8585	13572		2.15	2.6E-01	AF229118.1	NT
3983	8981	13986		0.94	2.6E-01	AW859610.1	EST_HUMAN
4031	8027	14016		17.72	2.6E-01	BE080588.1	EST_HUMAN
4231	8225	14208		1.2	2.6E-01	AF75283.1	NT
4417	8407	14394		1.2	2.6E-01	AA457617.1	EST_HUMAN
4512	8502	14481		2.55	2.6E-01	U01103.1	NT

Page 22 of 209

Table 4
Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4577	9365	14553	1.48	2.6E-01	AF142703.1	NT	Ophrestia radicosa matrasc-like protein (matrK) gene, complete cds; chloroplast gene for chloroplast product
4812	9796	14779	3.7	2.6E-01	HO46988.1	EST_HUMAN	Y51e05_r1 Soares placenta Nb2/HP Homo sapiens cDNA clone IMAGE:152288 5'
4877	6856			1.53	2.6E-01	AA884825.1	EST_HUMAN
5069	10038	15005	1.24	2.6E-01	M37701.1	NT	am33b11.11 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1468605 3'
239	6301	10311	1.57	2.5E-01	45022981	NT	Phrynosomium lignum peroxidase genes, complete cds
240	6301	10311	2.3	2.5E-01	45022981	NT	Homo sapiens ATP synthase, H+ translocating, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
253	6313		7.98	2.5E-01	M26501.1	NT	Homo sapiens ATP synthase, H+ translocating, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
822	5842	10978	0.98	2.5E-01	U099864.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
1043	6053		0.73	2.5E-01	AE002156.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1104	6111	11142	14.95	2.5E-01	789837.1	EST_HUMAN	Ureaplasma urealyticum section 57 of 69 of the complete genome
1690	6686		3.61	2.6E-01	4885406	NT	ye11077_r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117468 5'
1844	7757	11822	1.29	2.5E-01	BE69604.1	EST_HUMAN	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1844	7757	11823	1.29	2.5E-01	BE69604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
2342	7316		6.55	2.5E-01	AE000675.1	NT	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
2565	7528	12646	1	2.6E-01	X95310.1	NT	Aquifex aeolicus mRNA for D-ribofuranose oxidase
3328	8338		3.33	2.6E-01	AW973471.1	EST_HUMAN	B.taurus mRNA for D-ribofuranose oxidase
3457	8485	13492	1.12	2.6E-01	AF233975.1	NT	EST385484 IMAGE resequences, MAGM Homo sapiens cDNA
3473	8481	13600	6.31	2.6E-01	AI161617.2	NT	Danio rerio peptide YY precursor gene, complete cds
3757	8780	13759	1.65	2.5E-01	AI741483.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3757	8760	13760	1.65	2.5E-01	AI741483.1	EST_HUMAN	wg1c07_x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2384780 3'
3855	8953		1.09	2.5E-01	P32323	SWISSPROT	wg1c07_x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2384780 3'
4191	9184		0.91	2.5E-01	Q03314	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR RHIB PROTEIN
4606	8594		1.31	2.5E-01	Q27228	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4611	8597	14683	4.87	2.5E-01	AF007788.1	NT	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4637	8622	14614	2.24	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4658	9843		3.61	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and 5' segment of MuERV-L (murine endogenous retrovirus) element
4722	9707	14694	0.8	2.6E-01	UB8856.1	NT	Rattus norvegicus NF-KB gene, promoter region
549	6583	10585	1.12	2.4E-01	AA896316.1	EST_HUMAN	gn70d04_s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:15632023 3'

Page 23 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
838	5857	10898	1.73	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1285	6284	11328	14.3	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X73 gene and LZTFL1 gene
1285	6284	11327	14.3	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X73 gene and LZTFL1 gene
1814	6804			14.57	2.4E-01	AF267753.1	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1859	6848	11936	1.09	2.4E-01	AF261708.1	NT	Zacys duminae fructose-1,6-bisphosphatase mRNA, complete cds
2104	7084			1.04	2.4E-01	P46384	SWISSPROT
2200	7178	12301	1.88	2.4E-01	AE000680.1	NT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2320	7285	12415	131.89	2.4E-01	BF002171.1	EST_HUMAN	712304.x1 NC1_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3318807 3' similar to SW:PRSB_XENLA
2487	7436	12553	2.1	2.4E-01	Z36534.1	NT	O42588_26S PROTEASE REGULATORY SUBUNIT 6A;
2688	7646	12761	1.53	2.4E-01	X77783.1	NT	D discodeum (A3-K) ponA gene
2713	7670	12783	3.6	2.4E-01	AF030154.1	NT	S pombe swi5 gene
							Bovine adrenovirus 3 complete genome
3059	8078		3.61	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrof (peg/peg) genes, complete cds
3075	8091	13105	1.58	2.4E-01	X74209.1	NT	H sapiens ACT gene, PstI fragment of intron 4
3675	8680	13683	0.71	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
3920	8920		0.95	2.4E-01	D28616.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
4886	8960	14937	1.38	2.4E-01	AF252302.1	NT	Oncophrynichus mykiss shaker-related potassium channel Tshaz2 gene, complete cds
388	5426	10441	0.83	2.3E-01	S75898.1	NT	aromatase [Poecilia reticulata=zebra finches, ovary] mRNA, 3188 nt
631	5659		4.7	2.3E-01	U39713.1	NT	Mycobacteria genitalium section 35 of 51 of the complete genome
659	5696	10693	27.33	2.3E-01	U67598.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
921	6937	10988	3.41	2.3E-01	BE3111893.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1592	6588	11650	2.09	2.3E-01	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
1984	6978		1.08	2.3E-01	AJ235353.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2378	7350	12470	1.58	2.3E-01	BE297718.1	EST_HUMAN	50117552F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531016 5'
2579	7542	12656	0.92	2.3E-01	M11319.1	NT	Human erythropoletin gene, complete cds
2751	6362	11411	1.87	2.3E-01	AB015033.1	NT	Martinillabius agororovans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
2893	7912	12933	0.83	2.3E-01	AA601319.1	EST_HUMAN	no1606.61 NC1_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element;contains element THR repetitive element;
3010	8027		6.01	2.3E-01	R21732.1	EST_HUMAN	yh21b07.61 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3216	8231	13252	0.91	2.3E-01	U65391.1	NT	Lycopersicon esculentum PRF (Prf) gene, complete cds
3288	8289	13329	1.23	2.3E-01	H68836.1	EST_HUMAN	yr97h10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
3832	8834		5.26	2.3E-01	7682133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4224	8218	14197	6.38	2.3E-01	R82252.1	EST_HUMAN	Y17f01.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'

Page 24 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4277 9270			1.85	2.3E-01	LT8769.1	NT	Mus musculus reelin (Rer-1c) gene, promoter region
4328 9320	14305		0.87	2.3E-01	DP0869.1	NT	Synochocystis sp. PCC6803 complete genome, 1/27, 1-138899
4360 9351	14330		2.08	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (P38K/M13) mRNA, complete cds
4422 9412	14400		5.79	2.3E-01	60319824	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
4882 9861	14832		0.69	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
88 5165	10176		0.8	2.2E-01	A1052190.1	EST_HUMAN	oz14810.x1 Soares_fetal_liver_spleen_1NF1-S1 Homo sapiens cDNA clone IMAGE:1675280 3' similar to TR-013040 C13040 ATP-BINDING CASSETTE PROTEIN;
1532 6530	11690		2.42	2.2E-01	AF187650.1	NT	Homo sapiens PPAR delta gene, promoter region
1969 6954			1.16	2.2E-01	AF171901.1	NT	Trimeresurus malabaricus cypb gene, partial cds; mitochondrial gene for mitochondrial product
2035 7018	12128		1.86	2.2E-01	AM34640.1	NT	Fresh-water sponge Enm1 alpha collagen (COLF) gene
2339 7313	12434		4.2	2.2E-01	BF677538.1	EST_HUMAN	6020856608F NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248689 5'
2512 7480	12695		1.38	2.2E-01	BE618268.1	EST_HUMAN	601462528F NIH_MGC_67 Homo sapiens cDNA clone IMAGE:38668180 5'
2512 7480	12596		1.38	2.2E-01	BE618268.1	EST_HUMAN	601462529F NIH_MGC_67 Homo sapiens cDNA clone IMAGE:38668180 6'
2812 7832	12848		5.48	2.2E-01	BE1-55625.1	EST_HUMAN	PM2-HT0353-281289-003-612 HT0353 Homo sapiens cDNA
2812 7832	12849		6.48	2.2E-01	BE1-55626.1	EST_HUMAN	PM2-HT0353-281289-003-612 HT0353 Homo sapiens cDNA
2850 7870			1.44	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3308 8319			2.3	2.2E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
3687 8872	13676		1.51	2.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
3724 8728			1.61	2.2E-01	AF155728.1	NT	Xiphophorus maculatus truncated Rexti retrotransposon reverse transcriptase (RT) pseudogene
4091 8985			1.09	2.2E-01	AF119102.1	NT	Drosophila melanogaster U11C-119 (unc-119) gene, complete cds
4098 8982	14078		6.31	2.2E-01	AF15542.1	NT	Mus musculus mixed lineage kinase 3 (Mll3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4141 9136	14119		2.24	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4141 9136	14120		2.24	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4230 8924	14206		1.24	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4230 9224	14207		1.24	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4679 9864			1.4	2.2E-01	D50604.1	NT	Human beta-cytoplasmic actin (ACTBP1) pseudogene
4684 8869	14681		2.15	2.2E-01	AA211216.1	EST_HUMAN	za87c05.r1 Strategene hINT neuron (f#53723) Homo sapiens cDNA clone IMAGE:6486968 5'
4878 9887			1.24	2.2E-01	L13289.1	NT	Mus musculus vinculin gene, exon 3
							yr42n9.11 Soares_fetal_liver_spleen_1NF1-S1 Homo sapiens cDNA clone IMAGE:208001 6' similar to
4961 8938	14915		0.91	2.2E-01	HE0548.1	EST_HUMAN	9b:Z14116_m1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
856 5972	11008		1.5	2.1E-01	AA569289.1	EST_HUMAN	nm31e11.81 NC1_OGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
859 5974	11008		1.79	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18

Page 25 of 209
 Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1107	6113			2.1E-01 AE002314.2	NT		Chlamydia muridatum, section 45 of 65 of the complete genome
1119	6181	11217		2.1E-01	6754289	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1119	6181	11218		2.1E-01	6754289	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1889	6858	11846		1.52	2.1E-01 AA908824.1	EST_HUMAN	cl73e02.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1519810 3' similar to gb:K02765 COMPLEMENT C3 PRECURSOR (HUMAN);
2084	7075	12189		2.42	2.1E-01 BF695073.1	EST_HUMAN	602083128f1 NIH MGCC 81 Homo sapiens cDNA clone IMAGE:4247503 5'
2854	7874	12889		2.25	2.1E-01	6912445	NT
2718	8122			6.22	2.1E-01	9833861	NT
3940	89338	13930		1.28	2.1E-01 P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
3940	89338	13931		1.28	2.1E-01 P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4128	9123			0.9	2.1E-01 AF1124526.1	NT	Orchestia cavimana calcium-binding protein BP23 precursor (BP23) gene, complete cds
4251	9245			1.28	2.1E-01 AB033044.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4443	9433	14416		1.66	2.1E-01 AB010273.1	NT	Homo sapiens pshsp47 gene, complete cds
4719	9104	14680		4	2.1E-01 A10059794.1	NT	Homo sapiens hox11 proto-oncogene, exons 1 to 3 and hox-1 gene
5030	10001			0.92	2.1E-01 P265680	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN) (P22); ENVELOPE GLYCOPROTEIN E1 (GP32) (GP35); ENVELOPE GLYCOPROTEIN E2 (GP88) (GP70) (NS1); PROTEIN P7; NONSTRUCTURAL PROTEIN NS2 (P21) : PROTEASE/HELICASE NS3 (P7); NONSTRUCTURAL PROTEIN>
5067	10036	16003		1	2.1E-01 P02948.1	NT	Human surfactant protein-C (SP-C) gene, complete cds
200	5284	10278		2.64	2.0E-01 AB011437.1	NT	Galius galius mRNA for avb6, complete cds
530	5585			2.17	2.0E-01	7705601	NT
690	5744	10728		1.32	2.0E-01 M77085.1	NT	Homo sapiens CgI-18 protein (LOC51005), mRNA
801	5822	10852		6.78	2.0E-01 AF027885.1	NT	O. corniculus germline IgH heavy chain V-H pseudogene, allele type VH-1a2
988	6008	11038		0.68	2.0E-01 D90905.1	NT	Mus musculus Major Histocompatibility Locus class II region
1108	6114	11144		2.91	2.0E-01 AL163213.2	NT	Synechocystis sp. PCC6803 complete genome, 7/27, 781448-920975
1235	6233	11277		1.34	2.0E-01 AJ132685.6	NT	Homo sapiens chromosome 21 segment HS21C013
1289	6283	11332		1.08	2.0E-01 AW38927.1	EST_HUMAN	Homo sapiens rac1 gene
1432	6429			1.01	2.0E-01 AJ243987.1	NT	PM1/H0422-281289-202-c026 HT0422 Homo sapiens cDNA
1456	6453	11612		7.19	2.0E-01	45032408	Plum pox virus strain M, complete genome, isolate PS
1520	6517	11574		3.81	2.0E-01 AB007974.1	NT	Homo sapiens dystrobrevin, alpha (DINA), mRNA
1826	6523	11580		1.54	2.0E-01 AF260700.1	NT	Homo sapiens cholinesterase transporter mRNA, partial cds
1858	6654	11726		1.48	2.0E-01 U22346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1879	6875			1.48	2.0E-01 AF111170.3	NT	Homo sapiens 14q32.2 Jagged2 gene, complete cds; and unknown gene

Page 26 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1720	6715		3.96	2.0E-01	U67525_1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1853	6842	11830	0.93	2.0E-01	8922238	NT	Homo sapiens hypothetical protein FLJ10120 (FLJ10120), mRNA
2286	7262		1.21	2.0E-01	X82877_1	NT	H. sapiens Na+-D-Glucose cotransport regulator gene
3407	8418	13444	0.68	2.0E-01	P46807	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HB-ZIP PROTEIN ATHB-10)
3489	8497		0.67	2.0E-01	AW238005_1	EST_HUMAN	XP_15022_x1 NCI_CGAP_HNB Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element MER21 (repetitive element);
3624	8831	13637	0.7	2.0E-01	P34841	SWISSPROT	CED-11 PROTEIN
3919	8919	13912	0.77	2.0E-01	X83897_1	NT	C. parasitica espC gene
4433	9423		9.72	2.0E-01	BE829165_1	EST_HUMAN	QV4-EN0032-190502-223-603 EN0032 Homo sapiens cDNA
4874	9853	14828	7.34	2.0E-01	8922080	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
4921	9908	14885	0.83	2.0E-01	Y19216_1	NT	Homo sapiens putative pathHbD pseudogene for hair keratin, exons 1 to 9
4979	7840		7.46	2.0E-01	AF074890_1	NT	Homo sapiens full length insert cDNA YH85A11
5045	10016	14985	1.19	2.0E-01	AF167159_1	NT	Mus musculus cubilin mRNA, partial cds
5059	10029		1.29	2.0E-01	T47785_1	EST_HUMAN	Y017a10_r1 Sirene gene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:71418 5'
110	5182	8.3	1.9E-01		7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nucleic translocator 1 (Ant1), mRNA
350	5402	10412	5.34	1.9E-01	AF004353_1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
648	5676	10682	24.68	1.9E-01	U32681_12	NT	Homo sapiens lembda/loba protein kinase C-interacting protein mRNA, complete cds
648	5678	10683	24.68	1.9E-01	U32681_12	NT	Homo sapiens lembda/loba protein kinase C-interacting protein mRNA, complete cds
655	5683	10690	8.04	1.9E-01	BE070801_1	EST_HUMAN	RC3-BT0502-251189-011-d01 BT0502 Homo sapiens cDNA
656	5683	10690	5.32	1.9E-01	BE070801_1	EST_HUMAN	RC3-BT0502-251189-011-d01 BT0502 Homo sapiens cDNA
971	5986		0.66	1.9E-01	7305180	NT	Mus musculus Interleukin 2 receptor, gamma chain (IL2g), mRNA
1087	6094	11124	12.01	1.9E-01	AA358813_1	EST_HUMAN	EST67784 Fetal lung II Homo sapiens cDNA 5' end
1353	6350	11400	3.22	1.9E-01	AF061222_1	NT	Sorghum bicolor 22 kDa kafin cluster
1409	6407		2.64	1.9E-01	AF184623_1	NT	Plasmidium vivax reticulocyte binding protein-2 (bp-2) gene, complete cds
2319	7284	12414	2.22	1.9E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2852	7872	12887	3.81	1.9E-01	U66066_1	NT	Sigmodon hispidus 653 gene, partial cds
2868	7887		5.5	1.9E-01	J00922_1	NT	Galus gallus ovalbumin (Y) gene, complete cds
3311	8322	13345	4.28	1.9E-01	D13197_1	NT	Mouse gene for immunoglobulin diversity region D1
3399	8408	13434	4.85	1.9E-01	R16467_1	EST_HUMAN	Y4210_r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129547 5'
3716	8720	13721	0.77	1.9E-01	AF26407_1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
3746	8750	13749	1	1.9E-01	P30768	SWISSPROT	PAIRWISE PROTEIN ODD-PAIRED
3886	8887	13885	3.37	1.9E-01	AB006754_1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
3968	8967	13956	1.47	1.9E-01	AW754106_1	EST_HUMAN	CM3-C70315-271189-046-b11 CT0315 Homo sapiens cDNA

Page 27 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4110	9104	14080	1	1.8E-01	BE834643.1	EST_HUMAN	MR1-FN0010-290700-007-004 FN0010 Homo sapiens cDNA
4851	9853		1.11	1.8E-01	AF228642.1	NT	Ratius norvegicus chemokine receptor CXCR3 mRNA, complete cds
32	5112	10098	1.73	1.8E-01	U73200.1	NT	Mus musculus p116Rip mRNA, complete cds
258	7717	10327	1.97	1.8E-01	AB022290.1	NT	Mus musculus Cct gene for chaperonin containing TCP-1 gamma subunit, partial cds
							Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
369	5418	10433	1.48	1.8E-01	4502532	NT	
737	5760	10783	1.61	1.8E-01	AB021480.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OiGC1, complete cds
987	5982	11014	0.75	1.8E-01	AI912242.1	EST_HUMAN	wd7f02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2331051 3'
1075	6082	11112	1.17	1.8E-01	AF000580.1	NT	Dichotomium discoideum plasmid Ddp5, complete genome
1269	6207	11309	7.26	1.8E-01	AI117189.1	NT	Yersinia pestis plasmid pCD1
1810	6800		1.18	1.8E-01	4505036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1829	6819		1.34	1.8E-01	AI733708.1	EST_HUMAN	qg22d10.x5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:076836 Q75938 GAMMA BUTYROBETAINE HYDROXYLASE;
							Mus musculus Scyaf6, Scyaf6-ps, Scyaf6 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scyaf16 pseudogene, small inducible cytokine A5 precursor, complete cds
1871	6880	11948	1.42	1.8E-01	AB051897.1	NT	
2620	7582		1.63	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081298-036-004 DT0018 Homo sapiens cDNA
2827	7848		1.6	1.8E-01	AF184589.1	NT	Jonquilopsis aculeata LEAFY protein (LEAFY2) gene, partial cds
2833	7853	12873	1.28	1.8E-01	AW182301.1	EST_HUMAN	X414e03.x1 Soares, NEL-T GBC, S1 Homo sapiens cDNA clone IMAGE:2659766 3'
3051	8068	13077	2.5	1.8E-01	AW985178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3285	8296	13322	0.88	1.8E-01	BF183582.1	EST_HUMAN	601809728R11 NIH MGIC 18 Homo sapiens cDNA clone IMAGE:4040021 3'
3540	8546	13553	0.78	1.8E-01	H03369.1	EST_HUMAN	Y45601.81 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Ali repetitive element;
3540	8546	13554	0.78	1.8E-01	H03369.1	EST_HUMAN	Y45601.81 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Ali repetitive element;
4206	9199		1.21	1.8E-01	D37964.1	NT	Bovine NB26 mRNA for MHC class II (B6a-DQB), complete cds
4424	9414	14401	6.34	1.8E-01	AL161656.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
							Mus musculus Scyaf6, Scyaf6, Scyaf6-ps, Scyaf6 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scyaf16 pseudogene, small inducible cytokine A5 precursor, complete cds
4627	9612	14601	3.53	1.8E-01	AB051897.1	NT	
4651	9846	14634	1.89	1.8E-01	X92179.1	NT	S.tuberosum mRNA for alcohol dehydrogenase
4880	9859	14830	2.79	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151288-112-908 ST0203 Homo sapiens cDNA
4924	9901	14877	6.38	1.8E-01	AF181258.1	NT	Mesocricetus auratus Neutrochorelate coexpressing polypeptide mRNA, partial cds
4942	9919	14899	1.04	1.8E-01	AI438988.1	EST_HUMAN	II7604.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'

Page 28 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5061	10030	14997	0.83	1.8E-01	X50208.1	NT	<i>Escherichia coli</i> reverse transcriptase, retton EC86
5081	10030	14998	0.83	1.8E-01	X50208.1	NT	<i>Escherichia coli</i> reverse transcriptase, retton EC86
572	5605	10603	1.68	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3815768 6'
798	5817	10848	1.92	1.7E-01	X53330.1	NT	<i>P. duodenuli</i> histone gene cluster for core histones H2A, H2B, H3 and H4
846	5963		2	1.7E-01	P356168	SWISSPROT	NEUROFILAMENT TRIPLE T PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1041	6051	11080	1.31	1.7E-01	AF081810.1	NT	<i>Lymantria dispar</i> nucleopolyhedrovirus, complete genome
1041	6051	11081	1.31	1.7E-01	AF081810.1	NT	<i>Lymantria dispar</i> nucleopolyhedrovirus, complete genome
1781	6773	11865	1.64	1.7E-01	AL181513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment, No. 69
1935	6921		1.96	1.7E-01	AF255051.1	NT	<i>Homo sapiens</i> BNP13H (BNP13H) gene, complete cds; nuclear gene for mitochondrial product
2788	7809	12826	2.05	1.7E-01	AF000718.1	NT	<i>Vibrio cholerae</i> hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hpr) gene, complete cds, and YRAL_VIBCO gene, partial cds
2788	7809	12827	2.05	1.7E-01	AF000716.1	NT	<i>Vibrio cholerae</i> hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hpr) gene, complete cds, and YRAL_VIBCO gene, partial cds
2836	7876	12892	1.65	1.7E-01	AA336908.1	EST_HUMAN	EST41651 Endometrial tumor <i>Homo sapiens</i> cDNA 5' end
2928	7947	12984	1.1	1.7E-01	AJ238736.1	NT	<i>Neja neja</i> stra ctk-1 gene, exons 1-3
2928	7947	12985	1.1	1.7E-01	AJ238735.1	NT	<i>Neja neja</i> stra ctk-1 gene, exons 1-3
3032	8049	13058	1.45	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3363	8371	13391	1.56	1.7E-01	AJ269505.1	NT	<i>Anabaena</i> sp. ORF4 (partial), ORF3, ORF2, ORF1, adpF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3527	8533	13540	1.17	1.7E-01	AJ224877.1	NT	<i>Homo sapiens</i> nap1 gene, complete CDS
3835	8837	13843	6.17	1.7E-01	AJ235377.1	NT	<i>Homo sapiens</i> derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL-HRX gene fused to intron 5 of the AF-4/FEF1 gene
4428	9418		1.89	1.7E-01	X52836.1	NT	Schistoscoeca gregaria alpha repetitive DNA q57eg9x1 Scares fetal liver_spleen_1NFLS_S1 <i>Homo sapiens</i> cDNA clone IMAGE:1848808 3' similar to Schistoscoeca gregaria alpha repetitive DNA
4691	9676	14659	1.31	1.7E-01	AJ247635.1	EST_HUMAN	contains ORF, b1 ORF, repetitive element; Homo sapiens mRNA for KIAA0472 protein, partial cds
4932	9809	14886	8.76	1.7E-01	AB007941.1	NT	<i>Homo sapiens</i> inactivation kinase gene, exon 6 and 7
126	5194	10208	1.64	1.8E-01	AF217592.1	NT	<i>Y75f2.11</i> Scares placenta Nb2/FP <i>Homo sapiens</i> cDNA clone IMAGE:1365699 6'
671	7695	10705	1.11	1.8E-01	R31497.1	EST_HUMAN	hk28d12.51 NC1 CGAP_Co11 <i>Homo sapiens</i> cDNA clone IMAGE:1014839 3'
1474	6471	11629	1.07	1.6E-01	AA548863.1	EST_HUMAN	<i>Homo sapiens</i> homeobox protein OTX2 gene, complete cds
1490	6487	11542	2.68	1.8E-01	AF288117.1	NT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
1883	6872	11861	1.19	1.8E-01	P22063	SWISSPROT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
1938	6924		1.08	1.8E-01	U10334.1	NT	

Page 29 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2322	7768	12418	0.98	1.6E-01	X94232.1	NT	<i>H. sapiens</i> mRNA for novel T-cell activation protein
2422	7393	12514	1.22	1.6E-01	AB037729.1	NT	<i>Homo sapiens</i> mRNA for <i>KIAA1308</i> protein, partial cds
2821	7842	12859	10.97	1.6E-01	AF185589.1	NT	<i>Homo sapiens</i> cytochrome P450 3A4 (CYP3A4) gene, promoter region
2821	7842	12860	10.97	1.6E-01	AF185589.1	NT	<i>Homo sapiens</i> cytochrome P450 3A4 (CYP3A4) gene, promoter region
3548	8555	13562	1.16	1.6E-01	AJ003165.1	NT	<i>Populus trichocarpa</i> cv. Trichobet AB13 gene
3548	8555	13563	1.16	1.6E-01	AJ003165.1	NT	<i>Populus trichocarpa</i> cv. Trichobet AB13 gene
3685	8669	13652	0.73	1.6E-01	AE000586.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
3894	8894			2.51	1.6E-01	AE04413.1	NT
4202	9105	14177	10.56	1.6E-01	AF178680.1	NT	<i>Homo sapiens</i> apelin gene, complete cds
4334	9325			2.61	1.6E-01	AW9688601.1	EST_HUMAN
4340	9331			3.9	1.6E-01	8763319	NT
4788	9772	14755	1.47	1.6E-01	AA088343.1	EST_HUMAN	E221955 38, 855 BP SEGMENT OF CHROMOSOME XIV.; 284h09 s1 Streptomyces colon #937204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955
4810	9794	14776	1.19	1.6E-01	AJ0066356.1	NT	<i>Lycoperdon esculentum</i> RsaI fragment 2, satellite region
4810	9794	14777	1.19	1.6E-01	AJ0066356.1	NT	<i>Lycoperdon esculentum</i> RsaI fragment 2, satellite region
5029	10000	14973					LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 PRECURSOR (MEGALIN)
246	5309	10316	1.21	1.6E-01	P98158	SWISSPROT	(GLYCOPROTEIN 330)
246	5306	10317	1.38	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
582	7694			1.38	1.5E-01	AV711696.1	EST_HUMAN
582	7694			2.11	1.5E-01	AL163284.2	NT
774	5796	10824	1.39	1.5E-01	AJ251865.1	NT	<i>Homo sapiens</i> chromosome 21 segment H521C084
1080	6087	11118	1.81	1.5E-01	AJ251865.1	NT	<i>Homo sapiens</i> partial SL C22A2 gene for organic cation transporter (OCT2), exon 1
1086	6103			2.69	1.5E-01	I36125.1	NT
1197	6198	11234	0.7	1.6E-01	AW195516.1	EST_HUMAN	Xn38611-x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:26905085 3'
1226	6254	11285	2.85	1.5E-01	D26535.1	NT	Human gene for dihydrodipolipamide succinyltransferase, complete cds (exon 1-15)
1226	6254	11286	2.85	1.5E-01	D26535.1	NT	Human gene for dihydrodipolipamide succinyltransferase, complete cds (exon 1-15)
1451	6448	11609	1.47	1.5E-01	AF117340.1	NT	<i>Mus musculus</i> MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
2639	7599	12713	1.34	1.5E-01	BF695381.1	EST_HUMAN	602089265F1_NH1_MGIC_B1 Homo sapiens cDNA clone IMAGE:4247537 6'
2843	7863			1.06	1.5E-01	AW572516.1	EST_HUMAN
3274	8286	13310	4.64	1.5E-01	AA935049.1	EST_HUMAN	008805_s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:NM114333
3670	8675	13678	2.01	1.6E-01	U09884.1	NT	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN); Mus musculus ICR/ Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds

Page 30 of 209
Table 4
Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3684	8688	13691	1.04	1.5E-01	7108358	NT	[Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDHK1), nuclear gene encoding mitochondrial protein, mRNA
3775	8778	13782	2.39	1.5E-01	AW685983.1	EST_HUMAN	[HJ10106_x1] Searcs_NFL_T_GBC_S1_Homo sapiens cDNA clone IMAGE:2981411 3'
3937	8938	13829	0.86	1.5E-01	AW368659.1	EST_HUMAN	RC2-H-T0149-191099-012-009 HT0149 Homo sapiens cDNA
4059	9053	14040	8.83	1.5E-01	AL163284.2	NT	[Homo sapiens chromosome 21 segment HS21C084
4585	9573	14563	1.41	1.5E-01	BF687765.1	EST_HUMAN	[602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086223 5'
4607	7589	12713	2.83	1.5E-01	BF695381.1	EST_HUMAN	[602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
4840	8824	14789	1.66	1.5E-01	AL161580.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
297	5354		1.61	1.4E-01	AF009863.1	NT	[Homo sapiens T cell receptor beta locus, TCRBV8SSP to TCRBV21S2A2 region
899	5917		2.72	1.4E-01	D78638.1	NT	[Xenopus laevis mRNA for DNA (cytosine-5-) methyltransferase, complete cds
1240	6238		2.11	1.4E-01	T81884.1	EST_HUMAN	[ydb4c01_81] Scores fetal liver spleen 1NF1 S Homo sapiens cDNA clone IMAGE:1120322 3'
1709	6704		1.2	1.4E-01	6676980	NT	[Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1712	6701	11783	1.61	1.4E-01	AE001170.1	NT	Thermotoga maritima section 22 of 138 of the complete genome
1839	6925		8.74	1.4E-01	AA720315.1	EST_HUMAN	[ny72d07_81] NCI_CGAP_GCB1_Homo sapiens cDNA clone IMAGE:1283821 3'
2720	7677	12781	4.18	1.4E-01	AB33498.1	EST_HUMAN	[wm74d01_x1] NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
3464	8472		1.55	1.4E-01	BF541524.1	EST_HUMAN	[602013527F1 NCI_CGAP_BmB4 Homo sapiens cDNA clone IMAGE:4149126 6'
3803	8805	13811	1.17	1.4E-01	RS6232.21	EST_HUMAN	[ygb7a03_11] Scores Infant brain 1NIB Homo sapiens cDNA clone IMAGE:41487 5'
3803	8806	13812	1.17	1.4E-01	RS6232.21	EST_HUMAN	[ygb7a03_11] Scores Infant brain 1NIB Homo sapiens cDNA clone IMAGE:41487 5'
4050	8046	14034	11.16	1.4E-01	AL698094.1	EST_HUMAN	[b56c02_x1] NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4050	8046	14035	11.16	1.4E-01	AL698094.1	EST_HUMAN	[b56c02_x1] NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4115	9109	14084	3.6	1.4E-01	AE001170.1	NT	Thermotoga maritima section 22 of 138 of the complete genome
320	6315	10384	2.28	1.3E-01	4758467	NT	[Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
320	6315	10385	2.28	1.3E-01	4758467	NT	[Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
525	5560	10563	1.88	1.3E-01	AB01339.1	NT	[Homo sapiens gene for NBS1, complete cds
630	5838	10883	1.51	1.3E-01	AJ277606.1	NT	[Human calicivirus HU/NLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/83/UK
630	5838	10864	1.61	1.3E-01	AJ277606.1	NT	[Human calicivirus HU/NLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/83/UK
630	5838	10883	0.83	1.3E-01	X53330.1	NT	[P.dumerilli histone gene cluster for core histones H2A, H2B, H3 and H4
834	5853	10891	1.49	1.3E-01	AF39518.1	NT	[Rattus norvegicus A-kinase anchor protein mRNA, complete cds
883	6901	11049	1.51	1.3E-01	AL117078.1	NT	[Biotryd cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1010	6020		2.67	1.3E-01	AL115265.1	NT	[Biotryd cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1110	6116		1.71	1.3E-01	AV712487.1	EST_HUMAN	[AV712487 DCA Homo sapiens cDNA clone DCAAFF05 5'
1198	6197	11233	0.91	1.3E-01	AF46277.1	NT	[Homo sapiens adapter protein CMIS mRNA, complete cds
1418	6415						

Page 31 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1819	6905	11898	1.68	1.3E-01	AL1117078.1	NT	Bostrychus cinereus strain T4 cDNA library under conditions of nitrogen deprivation
2106	7088		0.97	1.3E-01	AJ243578.1	NT	Rhodopseudomonas acidophila pucB5, pucA5, pucB6, pucA6, pucB7, pucA8, pucB8 and pucC genes and ORF151
2228	7205		1.04	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-012 ST0173 Homo sapiens cDNA
2318	7293		2.79	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2510	7478	12593	1.78	1.3E-01	MB89198.1	NT	Carassius auratus Keratin type 1 mRNA, complete cds
3278	8290	13315	0.98	1.3E-01	AF1986779.1	NT	Homo sapiens transcription factor 1GHM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds, and L-type calcium channel $\beta 2$
3368	8376	13398	1.03	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydroxyacetonephosphate mRNA, complete cds
3639	8845	13651	0.81	1.3E-01	AP0000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/7)
3639	8845	13652	0.81	1.3E-01	AP0000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/7)
3882	8883		1.37	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
3938	5658	10683	1.73	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
3938	5658	10684	1.73	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
4016	9012		0.82	1.3E-01	AF020713.1	NT	Bacteriophage SPBC2 complete genome
4034	9030		4.19	1.3E-01	AV384341.1	EST_HUMAN	QV3-DT0018-0B1289-036-003 DT0018 Homo sapiens cDNA
4042	9038	14028	1.78	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose bisphosphate aldolase mRNA, complete cds
4061	9055	14042	18.31	1.3E-01	AW273741.1	EST_HUMAN	x123f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4187	9180		1.96	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21CQ80
4403	8394	14378	2.77	1.3E-01	BE272339.1	EST_HUMAN	601126096f1 NIH MGCG 9 Homo sapiens cDNA clone IMAGE:2980063 5'
4940	6947	14897	1.78	1.3E-01	AI432531.1	EST_HUMAN	f38c10.x1 NC1_CGAP_Pari1 Homo sapiens cDNA clone IMAGE:2120562 3'
382	5457	10474	9.01	1.2E-01	AI421744.1	EST_HUMAN	f35b02.x1 NC1_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2098939 3' similar to gb:U05760_mn1
421	5079		1.74	1.2E-01	U66912.1	NT	ANNEEXIN V (HUMAN)
543	5577		2.9	1.2E-01	AF039442.1	NT	Dicytostellum discoidatum ORF DG1016 gene, partial cds
1358	6355	11405	2.5	1.2E-01	AI149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1358	6355	11406	2.5	1.2E-01	AI149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1364	6361		3.68	1.2E-01	AV735249.1	EST_HUMAN	AV735249 cda Homo sapiens cDNA clone cdaAB11 5'
1477	6474		1.03	1.2E-01	AA887474.1	EST_HUMAN	gb48609_51 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16871
							Q16871 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR :

Page 32 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1591	6587	11649	1.16	1.2E-01	Q14934	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR (NF-ATC4)) (NF-AT13)
1611	65057	11871	2.24	1.2E-01	A1285402.1	EST_HUMAN	q16909.x1 NCI CGAP_E002 Homo sapiens cDNA clone IMAGE:1980553 3'
1731	6726		9.87	1.2E-01	X89211.1	NT	H sapiens DNA for endogenous retrovirus like element
1878	6865		3.06	1.2E-01	AW449388.1	EST_HUMAN	U1-H-B13-ak-4e-10-0-U1s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2118	7098	12211	2.31	1.2E-01	BT148490.1	EST_HUMAN	60182156771 NIH MGCC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
2514	7482	12598	1.4	1.2E-01	AW9861558.1	EST_HUMAN	QV3-BN0046-22030-128-f10 B10046 Homo sapiens cDNA
2769	7790	12812	1.4	1.2E-01	U18018.1	NT	Human ET1 enhancer binding protein (ET1-F) mRNA, partial cds
2832	7852	12872	2.31	1.2E-01	AI1720470.1	EST_HUMAN	est8c09.x1 Barslund colon hPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:LG5095
2864	7884	12804	3.25	1.2E-01	M16364.1	NT	600 RIBOSOMAL PROTEIN L30 (HUMAN); Human creatine kinase-B mRNA, complete cds
2838	7955	12873	0.9	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3169	8175	13198	1.83	1.2E-01	AW370668.1	EST_HUMAN	QV1-BT0259-261089-021-d05 BT0259 Homo sapiens cDNA
3183	8199		0.78	1.2E-01	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3442	8450	13476	0.67	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3442	8450	13477	0.67	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3525	8407		0.71	1.2E-01	Z89118.1	NT	Bacillus subtilis complete genome (section 16 of 21); from 2785131 to 3013540
4058	9052	14038	1.91	1.2E-01	Z54255.1	NT	P.clarkii mRNA, repeat region (ID 2MRT7)
4058	9052	14039	1.91	1.2E-01	Z54255.1	NT	P.clarkii mRNA, repeat region (ID 2MRT7)
4648	9833		0.92	1.2E-01	AF221633.1	NT	Rana ridibunda a filuillary adenylylate cyclase-activating polypeptide variant 2 precursor, mRNA, complete cds, alternatively spliced
4857	9838	14811	9.45	1.2E-01	BF577357.1	EST_HUMAN	6021351851 NIH MGCC_81 Homo sapiens cDNA clone IMAGE:4280165 5'
4937	9914	14892	3.98	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C0227
4937	9914	14893	3.98	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C0227
5057	10027		4.85	1.2E-01	Q57599	SWISSPROT	RIBONUCLEASE III (RNASE III)
660	5694	10594	0.74	1.1E-01	AL561003.1	EST_HUMAN	In1808.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2187983 3'
611	5638	10840	8.71	1.1E-01	AA569008.1	EST_HUMAN	nm08g11.s1 NCI CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X069985_m1
1037	6047	11077	1.16	1.1E-01	BF697308.1	EST_HUMAN	HEM E OXYGENASE 1 (HUMAN); 60212984751 NIH MGCC_56 Homo sapiens cDNA clone IMAGE:2286771 5'
1069	6077		1.46	1.1E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1141	7740	11177	3.28	1.1E-01	AV972168.1	EST_HUMAN	EST384142 MAGE resequences, MAGL Homo sapiens cDNA
1230	6229	11274	1.76	1.1E-01	D640041.1	NT	Synectochelys sp. PCC6803 complete genome, 23/27, 2888767-3002865
1488	8485	11840	1.79	1.1E-01	AI140363.1	EST_HUMAN	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
2250	7227		2.31	1.1E-01	6765216	NT	Mus musculus pre T-cell antigen receptor alpha (P ^{TCR}), mRNA

Page 33 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2468	7707			1.24 1.1E-01	6978876 NT		Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2782	7803	12820		1.07 1.1E-01	S82418.1	NT	Interleukin-12 p35 subunit [mice, Genomic, 700 nt, segment 4 of 5]
2983	7811	12895		0.83 1.1E-01	F03285.1	EST_HUMAN	HS3CRF022 normalized infant brain cDNA clone c-Tr023'
3287	8280			1.57 1.1E-01	6753231 NT		Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (CACNA1G), mRNA
3336	8346	13364		2.76 1.1E-01	BE393186.1	EST_HUMAN	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (CACNA1G), mRNA
3369	8377	13397		1.5 1.1E-01	X62135.1	NT	6013088678F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3411	8420	13449		1.26 1.1E-01	R86946.1	EST_HUMAN	6013088678F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3501	8509	13823		0.8 1.1E-01	Y07895.1	NT	Alu repetitive element, A. Immeritus gene for transposase
3619	8526			0.84 1.1E-01	P97384	SWISSPROT	ANXIN XI (CALCYCLIN-ASSOCIATED ANXININ 50) (CAP-50)
3621	8534	13639		1.44 1.1E-01	X52708.1	NT	G. gallus gene encoding non-histone chromosomal protein HM/G-14b, exons 4 and 6
3894	8591	13975		1.01 1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-280100-025-907 ST0280 Homo sapiens cDNA
3894	8591	13976		1.01 1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-280100-025-907 ST0280 Homo sapiens cDNA
4131	9126			0.98 1.1E-01	AF167066.1	NT	Drosophila melanogaster Karbach protein (karb) mRNA, complete cds
4505	8485	14473		0.98 1.1E-01	S44957.1	NT	Tapet=1=integral membrane protein TAP-A-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4685	9870	14632		1.09 1.1E-01	Y07695.1	NT	A. Immeritus gene for transposase
4856	9837			0.86 1.1E-01	AW026547.1	EST_HUMAN	wv14h0221 NC1_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2528555 3'
5002	9973			1 1.1E-01	8923317 NT		Homo sapiens hypothetical protein FLJ20342 (FLJ20342), mRNA
1182	6184			3.86 1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1253	6251	11282		1.81 1.0E-01	A1985489.1	EST_HUMAN	ws08601_x1 NC1_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.13 MER7. repetitive element;
1369	6368	11415		1.69 1.0E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3434	8442	13468		0.99 1.0E-01	BF033981.0	EST_HUMAN	601458301F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3859849 5'
3637	8643	13649		0.87 1.0E-01	BF239818.1	EST_HUMAN	6011608489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
3848	8850	13858		2.47 1.0E-01	BF365703.1	EST_HUMAN	QV2-N70048-160800-318-ed15 NT0048 Homo sapiens cDNA
4283	9275	14263		1.88 1.0E-01	AE002265.2	NT	Chlamydomonas pneumoniae AR39, section 91 of 94 of the complete genome
4423	8413			1.85 1.0E-01	AI792248.1	EST_HUMAN	ar3204_36 Geaster Wilts tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4574	9562	14550		1.74 1.0E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
4767	9751	14740		2.04 1.0E-01	AW952344.1	EST_HUMAN	EST364414 MAGE resequences, MAGB Homo sapiens cDNA
4967	8944	14921		0.93 1.0E-01	AL163247.2	NT	Home sapiens chromosome 21, segment 1 HS21C047
6022	9893			3.42 1.0E-01	BE881568.1	EST_HUMAN	601490286F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:3892842 5'
2714	7671	12784		1.21 8.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3453365 5'
2714	7671	12785		1.21 8.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3453365 5'

Page 34 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
3192	8208	13228	1.38	9.9E-02	AF098310.1	NT	Homo sapiens neuretin III-alpha gene, partial cds	
559	5593	141	9.8E-02	X86386.1	NT	O. sativa RAI my3C gene for alpha-amylase		
3072	8088	13101	4.03	9.8E-02	AF184274.1	NT	Deucus carota leucanthocyanidin dioxygenase 2 (LDOX2) mRNA, LDOX2 allele, complete cds	
4102	9086	14081	5.22	9.8E-02	AF257329.1	NT	Leptospirillum muculans beta-tubulin mRNA, complete cds	
4102	9086	14052	5.22	9.8E-02	AF257328.1	NT	Leptospirillum muculans beta-tubulin mRNA, complete cds	
1332	6330	13179	1.38	9.7E-02	AB005680.1	NT	Alce arborescens mRNA for NADP-malic enzyme, complete cds	
1560	6547		1.11	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA	
2169	7177	12300	1.44	9.7E-02	BE168860.1	EST_HUMAN	QV1-H10516-070300-095-a04 HT0516 Homo sapiens cDNA	
3875	8876		3.83	9.7E-02	QB87986	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)	
1966	69851	12054	0.92	9.8E-02	AI080721.1	EST_HUMAN	oz47d11.x1 Seacrest_NihIMfu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'	
1966	69851	12055	0.92	9.8E-02	AI080721.1	EST_HUMAN	oz47d11.x1 Seacrest_NihIMfu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'	
4219	8212	14181	5.54	9.6E-02	Z32686.2	NT	Proteus mirabilis fimbrial operon, strain Hi320	
4842	9825	14800	1.16	9.8E-02	AW866230.1	EST_HUMAN	EST378303 IMAGE sequences, MAGI Homo sapiens cDNA	
4972	89448	14926	0.97	9.8E-02	BF061729.1	EST_HUMAN	RC5-BT0254-031089-011-a03 BT0254 Homo sapiens cDNA	
3985	8983	13969	2.27	9.5E-02	AW982385.1	EST_HUMAN	CM2-BN0023-050200-087-712 BN0023 Homo sapiens cDNA	
4947	89244	14902	0.83	9.8E-02	UG8374.1	NT	Lycoperdon esculentum polygalacturonase isoenzyme 1 beta subunit gene, complete cds	
1797	6786	11877	2.69	9.4E-02	BF671063.1	EST_HUMAN	602150882F_NIH_MGC_811 Homo sapiens cDNA clone IMAGE:42919177 5'	
3788	8791	13786	5.14	9.4E-02	Z330589.1	NT	M_capticum DNA for CON1G MC073	
2820	7899		1.7	9.3E-02	4809280	NT	Homo sapiens BAU1-associated protein 3 (BAUAP3) mRNA	
2959	7978		6.91	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1) mRNA	
3182	8188	13222	2.33	9.3E-02	BF576511.1	EST_HUMAN	602133086F_NIH_MGC_811 Homo sapiens cDNA clone IMAGE:4288269 5'	
4029	8025	14012	3.03	9.3E-02	BF391943.1	EST_HUMAN	60286082F_NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'	
4029	8025	14013	3.03	9.3E-02	BF391943.1	EST_HUMAN	60286082F_NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'	
4595	9583	2.31	9.3E-02	AV73224.1	EST_HUMAN	AV732224_HTF_Homo sapiens cDNA clone HTTAUJA06 5'		
228	5291	10287	7.76	9.2E-02	U80315.1	NT	Molluscum contagiosum virus subtype 1, complete genome	
228	5291	10288	7.76	9.2E-02	U80315.1	NT	Molluscum contagiosum virus subtype 1, complete genome	
228	5291	10289	7.76	9.2E-02	U80315.1	NT	Molluscum contagiosum virus subtype 1, complete genome	
2166	7145		3.57	9.2E-02	RS41568.1	EST_HUMAN	yg88f071 Seacrest infant brain 1NIB Homo sapiens cDNA clone IMAGE:41618 5'	
3108	8122	13140	3.95	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDYMIS-SPECIFIC PROTEIN E4 (EPIDYMAL PROTEIN BE-20)	
3233	8248	13269	0.82	9.2E-02	AI453454.1	EST_HUMAN	nt08601.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:928136 3'	
3505	8513		1.06	9.2E-02	6765216	NT	Mus musculus pre T-cell antigen receptor alpha (Pcra) mRNA	
4116	9110		0.98	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-83, latency-associated transcript, promoter region	
4181	8174		0.72	9.2E-02	BE288722.1	EST_HUMAN	6009449865F_NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860178 5'	

Page 35 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4504	9494	14472	1.89	9.2E-02	X96402.1	NT	G. gallus M1b-CK gene
420	6078	10063	6.08	9.1E-02	X77665.1	NT	O. cuniculus k12 keratin gene
3585	8592		0.93	9.1E-02	AW372569.1	EST_HUMAN	PM2-BT0349-161289-001-102 BT0349 Homo sapiens chromosome 4, contig fragment No. 54
4357	9348	14328	1.84	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
							FOLEATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
735	5758	10780	4.53	9.0E-02	P15328	SWISSPROT	hvo39g10.x1_NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Aliu repetitive element;
1594	6590	11851	5.3	9.0E-02	BE220482.1	EST_HUMAN	HIV-1 p86c08-08 from USA envelope glycoprotein (env) gene, partial cds
2731	7608	12802	2.97	9.0E-02	AF38522.1	NT	HIV-1 p86c08-08 from USA envelope glycoprotein (env) gene, partial cds
2731	7608	12803	2.97	9.0E-02	AF38522.1	NT	HIV-1 p86c08-08 from USA envelope glycoprotein (env) gene, partial cds
3262	8275	13259	0.76	9.0E-02	AF279136.1	NT	Diclobostylum discoidium spore coat structural protein Sp25 (coleE) gene, complete cds
4175	9109	14167	0.87	9.0E-02	SB8757.1	NT	corticosteroid-binding globulin [Saimiri sciureus] (Squirrel monkeys, liver, mRNA, 1474 nt)
4175	9109	14158	0.87	9.0E-02	SB8757.1	NT	corticosteroid-binding globulin [Saimiri sciureus] (Squirrel monkeys, liver, mRNA, 1474 nt)
4294	9206	14274	0.91	9.0E-02	PS5268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
4533	8523	14510	2.08	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
5028	9999	14972	1.01	9.0E-02	Q24597	SWISSPROT	REGULATORY PROTEIN ZESTE
1411	6409	11487	1.4	8.9E-02	BF701593.1	EST_HUMAN	60212803072_NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285951 5'
1411	6409	11468	1.4	8.9E-02	BF701593.1	EST_HUMAN	60212803072_NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285951 5'
4078	8070		2.28	8.9E-02	AF286065.1	NT	Atrichum angustatum AtrenFin2 protein (AtranFin2) gene, partial cds
1355	6352	11402	1.5	8.9E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3807	8810	13816	1.16	8.8E-02	AA289128.1	EST_HUMAN	EST11595 (yeast) Homo sapiens cDNA 5' end
3924	8924		3.83	8.8E-02	Q002688	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 135 KDa SUBUNIT (TAFII-135) (TAFII-130) (TAFII-130)
1608	6604	11667	1.11	8.7E-02	AI167231.1	EST_HUMAN	ox65601.s1 Soares_NhHmFr_U_S1 Homo sapiens cDNA clone IMAGE:1661161 3'
3610	8617	13826	4.63	8.7E-02	UB2695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds, and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3610	8617	13627	4.63	8.7E-02	UB2695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds, and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4568	8556	14544	1.24	8.7E-02	AF176636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
4929	8906		1.08	8.7E-02	AE000895.1	NT	Methanobacterium thermophilicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome

Page 36 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1233	6231	11275	6.22	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region, segment 2/2
2182	7161	12281	1.3	8.6E-02	BE405687.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3114	8130	13149	3.35	8.6E-02	LO5468.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds
3559	8568		3.87	8.6E-02	AF153382.1	NT	Dichotomelium discoideum adenylyl cyclase (acrA) gene, complete cds
2333	7307	12428		1.85	8.5E-02	AE000852.1	Helicobacter pylori 26698, section 130 of 134 of the complete genome
2596	7776	12874	3.69	8.4E-02	W639330.1	EST_HUMAN	244811.11 Soares_fetal_hear_NbH119W_Homo sapiens cDNA clone IMAGE:343532 5'
4228	8222	14202		0.99	8.4E-02	AF257213.1	NT
4228	9222	14203	0.99	8.4E-02	AF257213.1	NT	Carica porcinea glycoprotein alpha-subunit mRNA, complete cds
3512	8520	13532		5.85	8.3E-02	PT5334	SWISSPROT
4559	8547	14532	0.83	8.3E-02	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
1360	6397		6.17	8.2E-02	Y08170.2	NT	Gallus gallus mRNA for for OBCAM protein gamma isoform
1465	6462	11621		2.51	8.2E-02	AF167077.2	NT
3000	8018			2.44	8.2E-02	AL163206.2	NT
3713	8717		1.37	8.2E-02	AL16498.2	NT	Arachis hypogaea DNA chromosome 4, contig fragment No. 10
3901	8901	13899	1.18	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4161	9166	14139		5.75	8.2E-02	PA48860	SWISSPROT
4161	9166	14140		5.75	8.2E-02	PA48960	SWISSPROT
4161	9166	14141		5.75	8.2E-02	PA48960	SWISSPROT
4909	9888	14861	3.34	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5027	9888	14971	1.29	8.2E-02	AU118930.1	EST_HUMAN	AU118930_HMBA1_Homo sapiens cDNA clone IMAGE:1008744 5'
1484	8481	11520	1.06	8.1E-02	AB017138.1	NT	Pseudomonas putida melonase decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdch, mdcl and mdcm genes), complete cds
5082	10031	14989	1.05	8.1E-02	AE004873.1	NT	Pseudomonas aeruginosa PA01, section 234 of 528 of the complete genome
6	7711	10072	4.12	8.0E-02	AW854653.1	EST_HUMAN	EST366723 IMAGE sequences, MAGC_Homo sapiens cDNA
1659	7752	11728	9.29	8.0E-02	D26535.1	NT	Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-15)
1659	7752	11729	9.29	8.0E-02	D26535.1	NT	Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-15)
1862	6851	11939	2.81	8.0E-02	BE067219.1	EST_HUMAN	PM3-B10347-17020-001-008_B10347_Homo sapiens cDNA
2400	7371		2.75	8.0E-02	BF248744.1	EST_HUMAN	601955548F1 NIH_MGC_57_Homo sapiens cDNA clone IMAGE:4075619 5'
2830	7850	12869	0.87	8.0E-02	AL445087.1	NT	Thermoplasmata acidophilum complete genome; segment 5/5
3126	8730	13728	0.73	8.0E-02	AW9668118.1	EST_HUMAN	EST378191 IMAGE sequences, MAGI_Homo sapiens cDNA
3958	8958		0.76	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4631	9818	14607	1.25	8.0E-02	A1434202.1	EST_HUMAN	131g02.X1 NCI CGAP_Gene4_Homo sapiens cDNA clone IMAGE:2132114 3'
4669	8854		7.08	8.0E-02	X72794.1	NT	M. musculus gene for gelatinase B
5080	5939	10871	0.87	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome

Page 37 of 209

Table 4
Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2109	7089	12203	2.54	7.9E-02	BE250008.1	EST_HUMAN	6009843191F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2956510 5' similar to gb:Z226876
2910	7829	12948	11.99	7.9E-02	AI592029.1	EST_HUMAN	60S RIBOSOMAL PROTEIN L38 (HUMAN);
3760	8763	13163	5.05	7.9E-02	6881044 NT		Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3760	8763	131764	6.05	7.9E-02	6881044 NT		Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4666	8651		1.4	7.9E-02	AB008018.1	NT	Arribalzaga italiana RXN24L mRNA, partial cds
1191	6182	11228	1.69	7.8E-02	AI793275.1	EST_HUMAN	cc659d02_y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570487 5' similar to contains L1_3 L1 repetitive element;
1191	6182	11229	1.69	7.8E-02	AI793275.1	EST_HUMAN	cc659d02_y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570487 5' similar to contains L1_3 L1 repetitive element;
2332	7308	12426	1	7.8E-02	AI7221942.1	NT	Sus scrofa telomerase RNA pseudogene
2332	7306	12427	1	7.8E-02	AI7221942.1	NT	Sus scrofa telomerase RNA pseudogene
3663	8668		1.25	7.8E-02	BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859893 5'
4914	8668		3.15	7.8E-02	BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859893 5'
5066	10035	15002	1.02	7.8E-02	AI418520.1	EST_HUMAN	tg18g12_x1 Soares_NFL_T_GBC_ST1 Homo sapiens cDNA clone IMAGE:2112070 3' similar to contains MER10_13 MER10 repetitive element;
3506	8514		2.61	7.7E-02	AI238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
3303	8314	13340	2.57	7.6E-02	BE614432.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634933 5'
3324	8334	13384	0.82	7.6E-02	AA286447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
776	5798	10826	1.86	7.5E-02	5802093 NT		Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
776	5798	10827	1.86	7.6E-02	5902093 NT		Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1877	6866	11954	1.16	7.5E-02	AI163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4377	9368	14348	0.92	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
474	5510	10523	1.1	7.4E-02	AW838547.1	EST_HUMAN	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
3514	8522	13633	0.77	7.4E-02	AI807885.1	EST_HUMAN	Wf43h01_X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4566	9554	14541	1.18	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4680	9635	14628	2.97	7.4E-02	6978442 NT		Rattus norvegicus Activin receptor like kinase 1 (Actrl1), mRNA
4784	9768	14752	1.75	7.4E-02	6878492 NT		Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchtrp), mRNA
486	6503	10514	1.23	7.3E-02	BE964961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
498	6503	10515	1.23	7.3E-02	BE964961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
678	5701	10709	3.86	7.3E-02	AE001789.1	NT	Trematoda maritima section 101 of 136 of the complete genome
1450	7748	11608	2.33	7.3E-02	AW8020281.1	EST_HUMAN	CMD-NN1004-130300-284-908 NN1004 Homo sapiens cDNA

Page 38 of 209
Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1808	7756		11.5	7.3E-02	AL1633022	NT	<i>Homo sapiens chromosome 21 segment HS21C102</i>
4838	9822		1.14	7.3E-02	U12283.1	NT	<i>Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds</i>
120	5190	10202	1.2	7.2E-02	AE000882.1	NT	<i>Methanobacterium thermoautotrophicum from bases 1029-155 to 1039934 (section 88 of 148) of the complete genome</i>
120	5190	10203	1.2	7.2E-02	AE000882.1	NT	<i>Methanobacterium thermoautotrophicum from bases 1029-155 to 1039934 (section 88 of 148) of the complete genome</i>
1446	6443	11501	1.67	7.2E-02	AL163301.2	NT	<i>Homo sapiens chromosome 21 segment HS21C101</i>
1446	6443	11502	1.67	7.2E-02	AL163301.2	NT	<i>Homo sapiens chromosome 21 segment HS21C101</i>
2478	7447		1.86	7.2E-02	U14794.1	NT	<i>Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds</i>
3791	8794	13789	1.82	7.2E-02	AW298322.1	EST_HUMAN	<i>U1-H-BW0-8H-a-05-0-U1.s1 NCI CGAP Sub6 Homo sapiens cDNA clone IMAGE:2732019 3'</i>
4220	9213	14192	5.17	7.2E-02	BF672307.1	EST_HUMAN	<i>60207757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'</i>
1863	6852	11940	1.58	7.1E-02	LO2290.1	NT	<i>Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds</i>
2225	7202		1.06	7.1E-02	AE004480.1	NT	<i>Pseudomonas aeruginosa PA01, section 451 of 528 of the complete genome</i>
2230	7207	12322	5.78	7.1E-02	BF208802.1	EST_HUMAN	<i>60167228F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092881 5'</i>
4997	9899	14946	1.09	7.1E-02	BE208576.1	EST_HUMAN	<i>rat1005.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823921 5' similar to gb:X52851 ms1 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN); gb:X52803 Mouse mRNA for cyclophilin (MOUSE);</i>
524	5559	10582	1.16	7.0E-02	Q07092	SWISSPROT	<i>COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR</i>
1470	8467		0.92	7.0E-02	X96677.1	NT	<i>M. arthaea Mict-1 gene</i>
1724	6719	11197	1.17	7.0E-02	AA056343.1	EST_HUMAN	<i>266104.51 Strategene colon (#837204) Homo sapiens cDNA clone IMAGE:509599 3'</i>
2960	7919	12993	2.25	7.0E-02	AW138152.1	EST_HUMAN	<i>U1-H-B11-acy-c-07-0-U1.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'</i>
3802	8805	13810	0.82	7.0E-02	AA1815438.1	EST_HUMAN	<i>af65a12.s1 Seares_teslis_NHT Homo sapiens cDNA clone 1375878 3' similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);</i>
3931	8931	13922	1.07	7.0E-02	BE070264.1	EST_HUMAN	<i>QV4-BT0407280100-090-#10 BT0407 Homo sapiens cDNA CM0-JM100-060309-270-a12 UM0001 Homo sapiens cDNA</i>
4017	9013		0.96	7.0E-02	AW792982.1	EST_HUMAN	<i>Centis familiaris Inducible nitric oxide synthase mRNA, complete cds</i>
4093	9087	14076	1.2	7.0E-02	AF077921.1	NT	<i>601816281F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4060071 5'</i>
4773	9757	14745	7.8	7.0E-02	BF7381987.1	EST_HUMAN	<i>Homo sapiens chromosome 21 segment HS21C010</i>
510	6545	10548	17.58	6.9E-02	AL163210.2	NT	<i>Homo sapiens chromosome 21 segment HS21C010</i>
510	6545	10549	17.58	6.9E-02	AL163210.2	NT	<i>Homo sapiens chromosome 21 segment HS21C010</i>
1913	8310		1.29	6.9E-02	45079688	NT	<i>Homo sapiens regulator of G_s-selective protein signaling (ZGAP1) mRNA, and translated products</i>
3703	8707	13709	1.03	6.9E-02	Q06364	SWISSPROT	<i>26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)</i>

Page 39 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3703	8707	19710	1.03	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 210T)
1843	6833	11820	1.06	6.8E-02	AA498759.1	EST_HUMAN	683002;1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1843	6833	11921	1.06	6.8E-02	AA498759.1	EST_HUMAN	683002;1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1865	6854	11942	3.07	6.8E-02	AF156873.1	NT	Hom sapiens putative hepatic transcription factor (WBSCR14) gene, complete cds
3027	8044	13053	1.01	6.8E-02	AA781896.1	EST_HUMAN	ai75a06_s1_Scores_testis_NHT_Homo sapiens cDNA clone 1376628 3'
3027	8044	13054	1.01	6.8E-02	AA781896.1	EST_HUMAN	ai75a06_s1_Scores_testis_NHT_Homo sapiens cDNA clone 1376628 3'
3027	8044	13055	1.01	6.8E-02	AA781896.1	EST_HUMAN	ai75a06_s1_Scores_testis_NHT_Homo sapiens cDNA clone 1376628 3'
1487	6495			1.66	6.7E-02	AF115538.1	NT
1864	6843	11831	1.32	6.7E-02	AJ220285.1	EST_HUMAN	Onychophytes mykiss TAP-1 protein (OnmyTAP-1) mRNA, OnmyTAP-1 allele, complete cds
3635	8641	13646	4.56	6.7E-02	P1278	SWISSPROT	HOMEBOX PROTEIN HOXA4 (HOXA4)
1330	6328	11376	1.14	6.6E-02	AJ735509.1	EST_HUMAN	ai2609_x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SW-1 LIN1_NYCCO_P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG_;
1252	6349	11369	0.98	6.6E-02	AF24516.1	NT	Drosophila melanogaster calcin mRNA, complete cds
2117	7097	12210	1.74	6.6E-02	AJ289241.1	NT	Mus musculus Capn12 gene for calpein 12, exons 1-21, three alternative transcripts
3382	8390	13413	9.7	6.6E-02	RB4306.1	EST_HUMAN	1418b10_s1_Scores_placenta_Nb2hP Homo sapiens cDNA clone IMAGE:139578 3'
3398	8406	13432	2.63	6.6E-02		7108357 NT	Hom sapiens mesothelin (MSLN), transcript variant 1, mRNA
3398	8406	13433	2.63	6.6E-02		7108357 NT	Hom sapiens mesothelin (MSLN), transcript variant 1, mRNA
3985	8963	13953	1.53	6.6E-02	AF260225.1	NT	Hom sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
4819	9803	14783	9.95	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
4819	9803	14784	9.95	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
577	5698	10608	2	6.6E-02	BF027839.1	EST_HUMAN	601671046FTNIH MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
972	5988	11022	3.15	6.5E-02			Hom sapiens E2F-like protein (LOC51270) mRNA
1368	6385	11414	2.48	6.5E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1697	6692	11768	1.65	6.5E-02	AE000764.1	NT	Aquifex aeolicus secilin 96 of 109 of the complete genome
570	5603	10601	1.52	6.4E-02	X95458.1	NT	A.carterae precursor of peridinin-chlorophyll-a-protein (PCP) gene
1695	6690	11765	0.96	6.4E-02	AE001177.1	NT	Thermogae maritima section 89 of 136 of the complete genome
1695	6690	11766	0.98	6.4E-02	AE001177.1	NT	Thermogae maritima section 89 of 136 of the complete genome
2946	7895	12884	1.88	6.4E-02	6986923	NT	Mus musculus histone deacetylase 6 (Hdac6) mRNA
4928	9805	14883	1.21	6.4E-02	AL163247.2	NT	Hom sapiens chromosome 21 segment HS21C047
1716	6711	11788	2.39	6.3E-02	AF10905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70 gene, partial cds; smrNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes

Page 40 of 209
Table 4
Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3523	8530			2.55	6.3E-02 P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
4128	9124	14108		3.54	6.2E-02 AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4212	9205			1	6.2E-02 AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNP) mRNA, complete cds
4450	9440			5.96	6.2E-02 Q62191	SWISSPROT	52 KD ROP PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO52) (RO52)
5016	9887	14863		1.68	6.2E-02 R56526.1	EST_HUMAN	Y897e12_s1 Soares infant brain 1NB Homo sapiens cDNA clone IMAGE:41477 3 similar to gb:X57198_cds1
254	5314	10324		3.38	6.1E-02 D16471.1	NT	TRANSCRIPTION ELONGATION FACTOR S-II (HUMAN); Human mRNA, Xq terminal portion
3885	8895			2.17	6.1E-02 U73325.1	NT	Arabidopsis thaliana K+ Inward rectifying channel protein (AKC1) gene, complete cds
5000	9871	14947		0.92	6.1E-02 Y12503.1	NT	S. cerevisiae mRNA for Man9-mannosidase
5018	8898			1.37	6.1E-02 A1220330.1	EST_HUMAN	Q980e0x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842470 3'
1243	6241	11282		0.88	6.0E-02 AE001777.1	NT	Thermolobosa maritima section 88 of 138 of the complete genome
2700	7657			2.19	6.0E-02 AB031289.1	NT	Mesocestoides cordi mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2866	6173	10183		0.91	6.0E-02 AA189730.1	EST_HUMAN	ZP78504_r1 Strategene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:6263310 5'
2866	5173	10184		0.91	6.0E-02 AA189730.1	EST_HUMAN	ZP78504_r1 Strategene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:6263310 5'
3158	8174	13198		1.62	6.0E-02 AA372376.1	EST_HUMAN	EST84286 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3158	8174	13197		1.62	6.0E-02 AA372376.1	EST_HUMAN	EST84286 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3549	8556			2.87	6.0E-02 BE98443.2	EST_HUMAN	601656150r1 NIH_3T3 Homo sapiens cDNA clone IMAGE:3878060 3'
229	6292	10300		6.97	5.9E-02 AW834719.1	EST_HUMAN	RC1-DT0001-290100-012-e10 D100011 Homo sapiens cDNA
2914	7833	12852		2.79	5.9E-02 AF180269.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
920	5936			3.97	5.8E-02 D90110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
1620	6617	11683		2.52	5.8E-02 Q617688	SWISSPROT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
2789	7810			0.94	5.8E-02 AJ223621.1	NT	Populus trichocarpa CC0A0MT1 gene, exon 1 to exon 5
3578	6586	13591		1.8	5.8E-02 AE001775.1	NT	Thermolobosa maritima section 87 of 138 of the complete genome
4228	8223	14204		5.55	5.8E-02 AW051827.1	EST_HUMAN	W24c02_X1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4229	9223	14205		6.65	5.8E-02 AW051827.1	EST_HUMAN	W24c02_X1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4416	9406	14382		4.67	5.8E-02 AI247505.1	EST_HUMAN	QH56101_r1 Soares fetal liver_spleen_1NFL_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:NM13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4416	9408	14383		4.67	5.8E-02 AI247505.1	EST_HUMAN	QH5601_r1 Soares fetal liver_spleen_1NFL_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:NM13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4441	9431			2.28	5.8E-02 AF096284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
4892	9984	14942		4.11	5.8E-02 7657006	NT	Homo sapiens dual adaptor of phosphotyrosine and 3'-phosphoinositides (DAPP1), mRNA

Page 41 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2983	8001	13013	1.08	5.7E-02	AI091644.1	EST_HUMAN	ai091644.1
2988	8016	13029	1.11	5.7E-02	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3625	8632			1.02	5.7E-02	AF001292.1	Chironomus thummi globin VIIA.1 (cit.7A.1), globin B.1 (cit.9.1), globin II-beta (cit.2beta), non-functional globin XII (cit.13R1), globin XI (cit.12) and globin XI (cit.11) genes, complete cds
3712	8716	13718	2.21	5.7E-02	AW986791.1	EST_HUMAN	EST13718
4546	8535			1.05	5.7E-02	MS8086.1	NT
1495	6493	11548	1.7	6.6E-02	AF094465.1	NT	Bos taurus lysozyme gene (cow 3), complete cds
2226	7203		1.01	6.6E-02	BEB04308.1	EST_HUMAN	Hydrocotyle rotundifolia ribosomal protein L16 (rp16) gene, intron; chloroplast gene for chloroplast product
4506	8498	14474	1.56	6.6E-02	AB0113100.1	NT	60149457812 NIH MIGC_70 Homo sapiens cDNA clone IMAGE:3896610 5'
4557	8545	14630	0.84	6.6E-02	AA280589.1	EST_HUMAN	Lycopersicon esculentum LE-ACS8 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
2683	7546	12860	4.77	6.6E-02	XE78892.1	NT	za-5c01.1s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
3143	8159	13181	3.85	5.5E-02	BT755501	EST_HUMAN	H.sapiens gene encoding Leautotinigen
4095	8089	14077	1.04	5.5E-02	LA1661.1	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
1270	6268		0.75	5.4E-02	AF157623.1	NT	Gallid herpesvirus mRNA fragment
2953	7972		0.93	5.4E-02	A1277468.1	NT	Homo sapiens HTRA serine Protease (PRSS11) gene, complete cds
3337	10056		6.65	5.4E-02	BE073468.1	EST_HUMAN	Oryza sativa Ibis-1 gene for putative Bowman-Birk trypsin inhibitor
1036	6046	11075	1.48	5.3E-02	AW391248.1	EST_HUMAN	RC5-BT0559-140200-012-003 BT0559 Homo sapiens cDNA
1036	6046	11078	1.48	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021289-002-009 ST0213 Homo sapiens cDNA
1476	6473	11531	7.24	5.3E-02	TS94755.1	EST_HUMAN	ye37f12.r1 Stratagene lung #937210 Homo sapiens cDNA clone IMAGE:1118851 5' similar to gb:K01506 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2424	7395	12516	1.9	5.3E-02	AI276408.1	NT	Pseudomonas putida KgsA gene
2872	7891	12913	0.82	5.3E-02	MS8411.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
2872	7891	12914	0.82	5.3E-02	MS8411.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3079	8095	13109	4.71	5.3E-02	AI276408.1	NT	Pseudomonas putida KgsA gene
4916	9894	14888	9.18	5.3E-02	MS80463.1	NT	Uta musculus caudal type homeobox-1 (cdx-1) gene, complete cds
2221	7198		66.89	5.2E-02	50318008	NT	Homo sapiens imprin A, alpha (PABA peptide hydrobase) (MEP1A) mRNA
3040	8057	13065	2.21	5.2E-02	AI277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3040	8057	13066	2.21	5.2E-02	AI277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4156	9161	14133	3.13	5.2E-02	U0132.1	NT	Human steroid hormone receptor Nsr-1 mRNA, complete cds
2303	7278		0.86	5.1E-02	AI134071.1	EST_HUMAN	DKFZp547D073_r1 547 (synonym: fibr1) Homo sapiens cDNA clone DKFZp547D073 5'
4845	9827		0.81	5.1E-02	AB0311740.1	NT	Homo sapiens PBl1 gene for salivary proline-rich protein P-B, complete cds

Page 42 of 208
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
479	5516	10528	1.87	5.0E-02	AF098604.1	NT	<i>Mus musculus</i> fatty acid amide hydrolase gene, exon 10
1185	6198	11223	12.28	5.0E-02	259104.1	NT	<i>Bacillus subtilis</i> complete genome (section 1 of 21); from 1 to 213080
1944	6930	12028	2.88	5.0E-02	PO2810	SWISSPROT	Salivary acidic proline-rich phosphoprotein 1/2 precursor (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-PIPIF-S) (PROTEIN A/PROTEIN C) CONTAINS PEPTIDE P-C]
2746	6987	11021	1.3	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP- β -glucuronosyltransferase (UGT2B15) mRNA, complete cds
3263	8276		1.24	5.0E-02	7305610	NT	<i>Mus musculus</i> Unc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3615	8523		1.04	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 87 of 163 of the complete genome
3800	8607	13616	7.08	5.0E-02	U12769.2	NT	Anthonomus nemoralis period clock protein homolog mRNA, complete cds
223	6285		30.11	4.9E-02	M14230.1	NT	Chicken 28-kDa a vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
368	5417	10431	2.47	4.9E-02	AF276948.1	NT	<i> Homo sapiens</i> ABCA1 (ABCA1) gene, complete cds
368	6417	10432	2.47	4.9E-02	AF275948.1	NT	<i> Homo sapiens</i> ABCA1 (ABCA1) gene, complete cds
2803	7823	12838	0.89	4.9E-02	U32636.1	NT	Zea mays phenylacene synthase (Y1) gene, complete cds
3217	8232	13253	1.52	4.9E-02	PS4258	SWISSPROT	DENTATORIBRAL-PALLIOOLYUSIAN ATROPHY PROTEIN
3480	8498		2.64	4.9E-02	AA188940.1	EST_HUMAN	ZG4812.3 (Strategene NT) neuron (#937233) Homo sapiens cDNA clone IMAGE:632828 3' similar to ZG4812.3; Strategene NT neuron (#937233) Homo sapiens cDNA clone IMAGE:632828 3' similar to contains Alu repetitive element; contains element M83R1 repetitive element;
3511	8518	13530	0.71	4.9E-02	AA400944.1	EST_HUMAN	Z278a03.51 Soares testis_NH ₂ Homo sapiens cDNA clone IMAGE:728428 3'
3511	8519	13531	0.71	4.9E-02	AA400944.1	EST_HUMAN	Z278a03.51 Soares testis_NH ₂ Homo sapiens cDNA clone IMAGE:728428 3'
4692	8677	14860	2.02	4.9E-02	AW167821.1	EST_HUMAN	1q56g10.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2832386 3'
4692	8677	14861	2.02	4.9E-02	AW167821.1	EST_HUMAN	1q56g10.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2832386 3'
328	5381	10380	1.13	4.8E-02	D16471.1	NT	Human mRNA_Xq terminal portion
329	5381	10380	2.65	4.8E-02	D16471.1	NT	Human mRNA_Xq terminal portion
485	5522	10531	8.84	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2211	7188	12309	1.27	4.8E-02	W51983.1	EST_HUMAN	Z249b02.s1 Soares senescent fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30938 LIPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3136	8152	13175	2.05	4.8E-02	X17144.1	NT	Tetrahymena oostara histone H3II and histone H4II intergenic DNA
268	5327	10338	1.22	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251186-003-005 HT0339 Homo sapiens cDNA
730	5753	10774	2.86	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1273	6271		0.71	4.6E-02	AI014255.1	EST_HUMAN	arm50d02.s1 Johnson frontal cortex Homo sapiens cDNA clone IMAGE:1535979 3' similar to TR:PR0533
1342	6339	11380	2.41	4.6E-02	AV727059.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTCBW001 5'
2418	7389	12809	2.09	4.6E-02	AW236023.1	EST_HUMAN	X124f03.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2894653 3' similar to SW:GRF1_HUMAN
2736	6327	10398	2.38	4.6E-02	BE163583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1
3416	7958	12976	0.76	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251189-003-005 HT0339 Homo sapiens cDNA
							6 1

Page 43 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4004	9000		0.86	4.6E-02	AF220365.1	NT	<i>Mus musculus</i> nucleolar RNA helicase II/Gu (ddx21) gene, complete cds
444	5481	10499	1.67	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1189	6200	11236	0.81	4.5E-02	AF005730.1	NT	<i>Marburg</i> virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1189	6200	11237	0.81	4.5E-02	AF005730.1	NT	<i>Marburg</i> virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1768	6760	11347	4.15	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2051	7033	12145	2.17	4.5E-02	AE03964.1	NT	<i>Xylella fastidiosa</i> , section 110 of 228 of the complete genome
3640	8646	13653	3.82	4.5E-02	AL163278.2	NT	<i> Homo sapiens</i> chromosome 21 segment HS21/C078
219	6292		3.85	4.4E-02	BE872733.1	EST_HUMAN	601652154F (NIH_MGC_82) <i>Homo sapiens</i> cDNA clone IMAGE:3936388 5'
2038	70222		3.33	4.4E-02	P31588	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2419	7390	12510	1.11	4.4E-02	AW875475.1	EST_HUMAN	QV2_P70012-010300-070-902 PT0012 <i>Homo sapiens</i> cDNA
3555	8562	13568	1.81	4.4E-02	AF159160.1	NT	<i>Myxococcus xanthus</i> serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4493	9483	14461	0.99	4.4E-02	AF109907.1	NT	<i> Homo sapiens</i> S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4493	9483	14462	0.99	4.4E-02	AF109907.1	NT	<i> Homo sapiens</i> S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
772	5794	10822	6.82	4.3E-02	AF003289.1	NT	<i>Microtus savii</i> myosin heavy chain FM3A (FM3A) mRNA, complete cds
3345	8354	13372	8.44	4.3E-02	AL163210.2	NT	<i> Homo sapiens</i> chromosome 21 segment HS21/C010
3575	8582		1.23	4.3E-02	AF060588.1	NT	<i> Homo sapiens</i> promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
812	5833	10866	1.73	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 <i>Homo sapiens</i> cDNA clone NT2RM2000020 5'
835	5874		1.9	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 <i>Homo sapiens</i> cDNA clone NT2RM2000020 5'
885	5903	10844	1.49	4.2E-02	AW003845.1	EST_HUMAN	wx34g01.x1 NCI_CGAP_Pit1 <i>Homo sapiens</i> cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291 L1 RETROPOSON, ORF2 mRNA; contains L1:13 L1 L1 repetitive element;
1682	6678		2.39	4.2E-02	AL445066.1	NT	Thermoplasma acidophilum complete genome, segment 4/5
3580	8587	13592	1.51	4.2E-02	P23051	SWISSPROT	TRANSFORMING PROTEIN MAF
4600	8588	14576	3.38	4.2E-02	BF342995.1	EST_HUMAN	602011705F-1 NCI_CGAP_Bm84 <i>Homo sapiens</i> cDNA clone IMAGE:4152672 5'
2605	7567	12682	1.08	4.1E-02	AE002330.2	NT	<i>Chlamydia muridarum</i> , section 60 of 85 of the complete genome
4347	8928		8.04	4.1E-02	AW883484.1	EST_HUMAN	QV1_NN0012-180400-164-106 NN0012 <i>Homo sapiens</i> cDNA
4954	8931		0.67	4.1E-02	X85880.1	NT	L monocytogenes type 3 partial lpp gene (strain 433)
1603	65599	11680	0.9	4.0E-02	AL675392.1	EST_HUMAN	wb98101.x1 NCI_CGAP_P728 <i>Homo sapiens</i> cDNA clone IMAGE:2313745 3'
3170	8186	13207	3.01	4.0E-02	AB04004.1	NT	<i> Homo sapiens</i> mRNA for KIAA1471 protein, partial cds
1103	6110	11141	3.41	3.9E-02	BF516149.1	EST_HUMAN	Ui-H-BW ⁺ -anxh-08-0-U1, st1 NCI_CGAP_Sub7 <i>Homo sapiens</i> cDNA clone IMAGE:3084134 3'
1326	6324	11371	1.9	3.8E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
1821	6907	12001	1.85	3.9E-02	AJ403386.1	NT	<i>M.musculus</i> DNA for desmin-binding fragment DesD7

Page 44 of 209
Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe Seq ID NO:	Exon Seq ID NO:	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2632	7692	11025	1.51	3.9E-02	45068862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
977	6992	12274	6.31	3.7E-02	P19137	SWISSPROT	LAMININ ALPH-1 CHAIN PRECURSOR (LAMININ A CHAIN) wr8560B_x1 NCBI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2175	7154	12274	5.07	3.7E-02	AIR84808.1	EST_HUMAN	Homo sapiens mRNA for KIAA0718 protein, partial cds
2602	7470	12586	1.04	3.7E-02	AB018281.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
2976	7894	13008	1.04	3.7E-02	P78944	SWISSPROT	LEOMESODERMIN
2978	7995	13009	3.76	3.7E-02	BF312983.1	EST_HUMAN	601886233F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4126584 5'
3372	8380		1.16	3.7E-02	6680541	NT	<i>Mus musculus</i> potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnme3), mRNA
3115	8131	13150	43.98	3.6E-02	AP00003.1	NT	<i>Pyrococcus horikoshii</i> OT3 genomic DNA, 544001-77700 nt, position (37)
3570	8577	13583	0.8	3.6E-02	X73221.1	NT	<i>H. vulgare</i> Ss1 gene for sucrose synthase
3578	8585	13590	0.73	3.6E-02	AL086808.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
884	6902	10943	1.6	3.5E-02	UJ09506.1	NT	<i>Drosophila melanogaster</i> Igf1 mRNA, complete cds
983	80018	11037	1.11	3.5E-02	AF283417.1	NT	<i>Homo sapiens</i> microsomal epoxide hydrolase (EPHX1) gene, complete cds
1531	65229	11688	1.01	3.5E-02	BF678085.1	EST_HUMAN	60208513SF1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3249377 5'
1531	65229	11589	1.01	3.5E-02	BF678085.1	EST_HUMAN	60208513SF1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3249377 5'
4092	90866	14075	3.28	3.5E-02	AE001773.1	NT	<i>Thermatoga maritima</i> section 85 of 136 of the complete genome
4189	9182	14165	1.13	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
573	5606	10604	1.18	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
573	5606	10605	1.18	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
574	5606	10604	4.61	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
574	5606	10605	4.61	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1034	6044	11073	3.13	3.4E-02	AW274020.1	EST_HUMAN	x126d07_x1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW.C211_HUMAN_P33801_PUTATIVE_SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR :
1187	6168		9.31	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA yc20e06_r1 Strategene lung (R837210) Homo sapiens cDNA clone IMAGE:81280 5' similar to contain M1ER28 repetitive element
2328	7302	12422	1.86	3.4E-02	T57160.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C008
3346	8355	13313	1.39	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3688	8692	13694	0.7	3.4E-02	BE32914.1	EST_HUMAN	IRC3-FN0155-060700-011-410 FN0155 Homo sapiens cDNA
3821	8823	13830	3.3	3.4E-02	AW784952.1	EST_HUMAN	IRC8-UW0016-210200-021-A10 UW016 Homo sapiens cDNA
4467	9457	14437	3.07	3.4E-02	X59789.1	NT	M.musculus S-antigen gene promoter region
4892	8871		2.79	3.4E-02	Q26457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)

Page 45 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4806	9885	14856	1.61	3.4E-02	AF012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
371	6420		15.62	3.3E-02	AA398735.1	EST_HUMAN	Zf7608.s1 Scares testis. NIH Homo sapiens cDNA clone IMAGE:728168 3'
1149	6153	11185	14.2	3.3E-02	AB03887.1	NT	Cricetomys griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1699	6595	11656	1.34	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2031	7014		1.65	3.3E-02	R09112.1	EST_HUMAN	Yf25c09.r1 Scares fetal liver spleen 1NEf.5 Homo sapiens cDNA clone IMAGE:127838 5'
4053	6595	11656	2.72	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4343	9334	14318	2.06	3.3E-02	9755862	NT	Mus musculus tumor rejection antigen gp96 (Trat), mRNA
132	6198	10214	2.62	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding lissotin-dependent bile acid transporter
1109	6115	11145	14.14	3.2E-02	AF086275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1109	6115	11146	14.14	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2060	7042		8.6	3.2E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
3061	8078	13091	13.22	3.2E-02	BE887353.1	EST_HUMAN	601442431f NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'
3632	8638	13644	1.3	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
3854	8856	13861	0.89	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
3854	8856	13862	0.88	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
4097	8091		17.68	3.2E-02	X94768.1	NT	H.sapiens RP3 genes (XLRP gene 3)
4622	8607	14595	3.39	3.2E-02	AF114182.1	NT	Sedifugae nidifica mutase (mnk) gene, chloroplast gene encoding chloroplast protein, partial cds
4681	9886	14848	2.57	3.2E-02	AF087083.1	NT	Vitreoscilla sp. outer membrane protein homolog gene, complete cds; Tip repressor binding protein gene, partial cds; and unknown genes
1241	6239		1.62	3.1E-02	4503416	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1286	6285	11328	1.44	3.1E-02	P-8846	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GE-ALPHA-3)
1852	6841	11929	0.85	3.1E-02	6671594	NT	Mus musculus adaptor-related protein complex AP-3 delta subunit (Ap3d), mRNA
4998	9117		12.58	3.1E-02	AU118006.1	EST_HUMAN	AU118006 HEMBA1 Homo sapiens cDNA clone HEMBA1004842 5'
5072	10041		5.51	3.1E-02	5730074	NT	Homo sapiens fibroinger-like 2 (FGL2), mRNA
1584	6581		11.29	3.0E-02	AF187125.1	NT	Phytokleines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2509	7477	12532	0.99	3.0E-02	AA02242.1	EST_HUMAN	Zf85n03.r1 Scares testis. NIH Homo sapiens cDNA clone IMAGE:727253 5'
3486	8484	13611	0.95	3.0E-02	MB01176.1	NT	Saccharomyces cerevisiae stem-loop mutation suppressor SSI2 gene, complete cds
3569	8576	13592	2.92	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II amidotransferase gene, complete cds
3660	8865		0.72	3.0E-02	AW820223.1	EST_HUMAN	QV2-S10286-150200-040-049 ST0286 Homo sapiens cDNA
4885	9884	14834	7.12	3.0E-02	AF281074.1	NT	Homo sapiens neuroillin 2 (NRIP2) gene, complete cds; alternatively spliced
4885	9884	14835	7.12	3.0E-02	AF281074.1	NT	Homo sapiens neuroillin 2 (NRIP2) gene, complete cds; alternatively spliced

Page 46 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2368	7769	12459	1.06	2.9E-02	AF228703.1	NT	Hom sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
3827	8829	13836	1.37	2.9E-02	HT2805.1	EST_HUMAN	Y07e10.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
3877	8878	13881	0.73	2.9E-02	O15440	SWISSPROT	MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 5 (ABC TRANSPORTER MOAT-C) (PABC11) (SMRP)
4858	9839	14812	1.81	2.9E-02	X65137.1	NT	S. vulgaris pepC gene for PEP carboxylase
4858	9839	14813	1.81	2.9E-02	X65137.1	NT	S. vulgaris pepC gene for PEP carboxylase
2406	7377		1	2.8E-02	AA782516.1	EST_HUMAN	al55c08_s1 Soares_parallel_tumor_NibHPA Homo sapiens cDNA clone 1360912 3'
3286	8287	13323	1.1	2.8E-02	AF086033.1	NT	Hom sapiens retinal fascin (FSCN2) gene, exon 2
3286	8287	13324	1.1	2.8E-02	AF086033.1	NT	Hom sapiens retinal fascin (FSCN2) gene, exon 2
4185	9178		0.8	2.8E-02	8353757	NT	Reitius norvegicus microtubule-associated protein tau (Mapt), mRNA
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV2/TS1P, TCRBV22S1A2N1T, TCRBV8S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S1P, TCRBV7S3A2T, TCRBV15S2A1T, TCRBV8S2A2P1, TCRBV7S2A1N4T, TCRBV13S9/13S2
1457	8454	11513	1.09	2.7E-02	U68059.1	NT	Arabidopsis thaliana chromosome 4, contig fragment No. 8
3347	8356	13374	1.84	2.7E-02	AL161094.2	NT	Y066h12.11 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:280487 5'
4079	9073	14080	2.12	2.7E-02	NA47258.1	EST_HUMAN	Y066h12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:280487 5'
4079	9073	14081	2.12	2.7E-02	NA47258.1	EST_HUMAN	Y069f04_s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120127 3' similar to contains Alu repetitive element
5040	10011	14980	1.04	2.7E-02	T96073.1	EST_HUMAN	Hom sapiens chromosome 21 segment HS21C082
566	5599	10598	0.98	2.6E-02	AL163282.2	NT	II.3-C70219 Homo sapiens cDNA
1350	6347		0.83	2.6E-02	AW850515.1	EST_HUMAN	ab02b02_s1 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:839555 3'
2305	7280	12398	1.97	2.6E-02	AA89021.1	EST_HUMAN	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2307	7282	12400	1.99	2.6E-02	6754241	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70 mRNA and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes
2845	7885		1.39	2.6E-02	AF09896.1	NT	Chicken dorsalin-1 mRNA, complete cds
4749	9734	14720	3.57	2.6E-02	L12032.1	NT	M. musculus DNA for vimentin-binding fragment VimE7
4759	9743	14728	1.27	2.6E-02	AJ403239.1	NT	M. musculus DNA for vimentin-binding fragment VimE7
4759	9743	14729	1.27	2.6E-02	AJ403239.1	NT	Deinococcus radiodurans R1 section 151 of 228 of the complete chromosome 1
4897	9876	14844	1.74	2.6E-02	AEG02014.1	NT	X52b04_x1 NCI_CGAP_Ser4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW.Y059_HUMAN Q15041 HYPOTHETICAL PROTEIN KIAA0089
4921	9899	14874	2.61	2.6E-02	AW241164.1	EST_HUMAN	Q128f06_y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
523	6563	10566	1.4	2.5E-02	AI739130.1	EST_HUMAN	Q128f06_y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'

Page 47 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
528	6563	10567	1.4	2.5E-02	AI793130.1	EST_HUMAN	on26106.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
800	6821	10861	12.78	2.5E-02	BE874314.1	EST_HUMAN	801680305R2 NIH_MGG_83 Homo sapiens cDNA clone IMAGE:3950865 3'
858	6877	10918	4.21	2.5E-02	BE874314.1	EST_HUMAN	801680305R2 NIH_MGG_83 Homo sapiens cDNA clone IMAGE:3950865 3'
2689	7847		1.83	2.5E-02	U12571.1	NT	Rattus norvegicus (rabphilin-3A) mRNA, complete cds
2885	7804	12824	3.25	2.5E-02	X98697.1	NT	H_catherae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
2885	7904	12926	3.25	2.5E-02	X98697.1	NT	H_carteriae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
3932	10049	13923	0.85	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-#12 NN0128 Homo sapiens cDNA
3932	10049	13924	0.85	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-#12 NN0128 Homo sapiens cDNA
4083	9077	14085	5.51	2.5E-02	AW592114.1	EST_HUMAN	h36n08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834015 3'
173	6231	10249	0.68	2.4E-02	A1378582.1	EST_HUMAN	ts72c07_x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2070166 3'
1563	65560	116222	1.88	2.4E-02	H658884.1	EST_HUMAN	y75f11.r1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211149 6'
1993	77680	12082	1.31	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
1993	77680	12083	1.31	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4243	9243	14220	1.46	2.4E-02	I05110.1	NT	T_thermophiles calcium-binding 25 kDa (TCPB_25) protein mRNA, complete cds
4390	9381	14362	1.58	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4390	9381	14363	1.58	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
1834	6824		3.68	2.3E-02	W05340.1	EST_HUMAN	zeb4q08.1r1 Soares_fetal lung_NbHL19W Homo sapiens cDNA clone IMAGE:289294 5'
1848	6837		5.18	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2289	7284	12382	1.88	2.3E-02	Z74298.1	NT	S_cerevisiae chromosome IV reading frame ORF YDI245c
3598	8605	13613	5.37	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH_P_Human Brain White matter tissue Homo sapiens cDNA
4026	9022	14009	0.78	2.3E-02	L24798.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4026	9022	14010	0.78	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4296	9288	14276	1.14	2.3E-02	AW889107.1	EST_HUMAN	CMA-NN080-290400-160-504 NN0080 Homo sapiens cDNA
4327	9319	14301	0.85	2.3E-02	BE95225.1	EST_HUMAN	CMA-MT0118-010900-318-901 MT0118 Homo sapiens cDNA
4327	9319	14302	0.85	2.3E-02	BE95225.1	EST_HUMAN	CMA-MT0118-010900-318-907 MT0118 Homo sapiens cDNA
4328	10051	14303	0.82	2.3E-02	AW586893.1	EST_HUMAN	xs25d03.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4328	10051	14304	0.82	2.3E-02	AW586893.1	EST_HUMAN	xs25d03.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4483	9453	14434	2.76	2.3E-02	BF028487.1	EST_HUMAN	601672279F1 NIH_MGG_20 Homo sapiens cDNA clone IMAGE:395396 5'
4463	9453	14435	2.76	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGG_20 Homo sapiens cDNA clone IMAGE:3865386 5'
4860	9841		0.95	2.3E-02	7662173	NT	Homo sapiens KIAA0547 gene product (KIAA0547), mRNA
4977	9953	14931	0.77	2.3E-02	AF287110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
4977	9953	14932	0.77	2.3E-02	AF287110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
728	5751	10772	2.95	2.2E-02	AF018287.1	NT	Columba livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds

Page 48 of 209
 Table 4
 Single Exon Probes Expressed in HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1708	6703			2.2E-02	4557448	NT	Homo sapiens chromosomal helicase DNA binding protein 2 (CHD2) mRNA
1723	6718	11785	1.21	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1723	6718	11798	0.97	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1865	6950	12053	1.49	2.2E-02	Z82001.1	NT	<i>S. pneumoniae</i> popA gene and open reading frames
3350	8356		1.88	2.2E-02	AA577785.1	EST_HUMAN	<i>Han24e04_s1_NCI</i> CGAP <i>Gast</i> Homo sapiens cDNA clone IMAGE:1084782 3'
3561	8568		3.57	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3763	8768	13769	1.18	2.2E-02	AW601317.1	EST_HUMAN	PM0-B10340-1710100-004-b03 BT0340 Homo sapiens cDNA
3820	8822	13829	0.68	2.2E-02	Z74283.1	NT	<i>S.cerevisiae</i> chromosome IV reading frame ORF YDL245c
416	5453		4.33	2.1E-02	AV761502	MDS_Homo sapiens cDNA clone MDSADG07 6'	
446	5483		7.77	2.1E-02	AF029728.1	NT	Dicytostelium discoideum histidine kinase C (dhkC) mRNA, complete cds
1244	6242	11283	7.23	2.1E-02	U72073.1	NT	<i>Bacillus substillis</i> colKLM cluster, ColK (colK), ColL (colL), and spor coat protein ColM (colM) genes, complete cds
1744	6739	11818	1.17	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1744	6739	11817	1.17	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1744	6739	11818	1.17	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2744	5792	10820	3.7	2.1E-02	NP_92866.1	EST_HUMAN	YK43107.r1 Soares melanocyte 2NbHm Homo sapiens cDNA clone IMAGE:786121 5'
3502	8510	13524	0.94	2.1E-02	AA461271.1	EST_HUMAN	ZK83b09.r1 Soares, total_fetus Nb2Hf8_9W Homo sapiens cDNA clone IMAGE:786124 5c
4009	8005	13983	0.87	2.1E-02	U74283.1	NT	<i>S.cerevisiae</i> chromosome IV reading frame ORF YDL245c
4182	9175	14159	0.8	2.1E-02	BT343655.1	EST_HUMAN	6020163036F_NCI CGAP Bm64 Homo sapiens cDNA clone IMAGE:4151161 5'
4322	9314	14287	1.92	2.1E-02	U44914.1	NT	Biorellia burgdorfensis plasmid cp32-2, <i>erpC</i> and <i>erpD</i> genes, complete cds; and unknown genes
4333	9324	14310	1.35	2.1E-02	AI7581127.1	EST_HUMAN	wg81d11_x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4540	9358		0.68	2.1E-02	Y19213.1	NT	Homo sapiens putative psf1/DA pseudogene for hair keratin, exons 2 to 7
4572	9560	14549	6.38	2.1E-02	Y6561.1	NT	<i>A.thaliana</i> mitochondrial genome, part A
4591	9579	14569	0.76	2.1E-02	AA665737.1	EST_HUMAN	leg55g12.51 Geissler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
17	5097	10080	1.78	2.0E-02	BF002982.1	EST_HUMAN	7851c08_x1 NCI CGAP_P728 Homo sapiens cDNA clone IMAGE:3308988 3 - similar to contains MER1.13
18	5098	10081	9.9	2.0E-02	AW895665.1	EST_HUMAN	MER1 repetitive element;
257	6317	10326	2.81	2.0E-02	6753635	NT	Mus musculus Dlb homolog 1 (E. col) (Dlb1), mRNA
293	6350	10363	1.85	2.0E-02	AA458638.1	EST_HUMAN	aa15b10_r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
790	5811	10841	1.4	2.0E-02	6753635	NT	Mus musculus Dlb homolog 1 (E. col) (Dlb1), mRNA
1071	6079	11110	1	2.0E-02	AL09805.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 11[1p38.33] of Homo sapiens
1180	6182	11219	1.31	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1180	6182	11220	1.31	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA

Page 49 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1835	8825	11912	1.69	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1835	8825	11913	1.69	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2726	7683		1.8	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3005	5097	10080	1.68	2.0E-02	BF002932.1	EST_HUMAN	7951c08_x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3309888 3' similar to contains MER1.13 MER1 repetitive element;
3071	8087		2.21	2.0E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sem6b), mRNA
3156	8172		1.54	2.0E-02	AF098558.1	NT	Arabidopsis thaliana C2h12 zinc finger protein F2F mRNA, complete cds
3900	8900	13698	1.81	2.0E-02	M18085.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
4943	8920		0.84	2.0E-02	AI271985.1	EST_HUMAN	Q83603_x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1866076 3'
684	5708	10720	1.76	1.8E-02	AA572764.1	EST_HUMAN	nr19a07_s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:9141986 similar to contains L1.L1 repetitive element;
1988	6973	12077	2.16	1.8E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
1988	6973	12078	2.18	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2434	7405	12623	1.18	1.9E-02	AL16150.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2835	7885	12874	7.79	1.9E-02	AA71356.1	EST_HUMAN	nw04f05_s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
2881	7800	12822	1.87	1.9E-02	AV648689.1	EST_HUMAN	AV648689 GLC Homo sapiens cDNA clone GLCBLH07 3'
3185	8201		0.75	1.9E-02	AB033611.1	NT	Urothorus talpoides mitochondrial gene for cytochrome b, complete cds
3530	8536	0.91	1.9E-02	AI52250.1	EST_HUMAN	y228b02_s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284331 3'	
3622	8629		8.78	1.9E-02	BE738088.1	EST_HUMAN	601672882F NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3339564 5'
3633	8639	13645	0.74	1.9E-02	AI301183.1	EST_HUMAN	qnr04c07_x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element;
3834	8939	13929	1.5	1.9E-02	AF141940.1	NT	Mycoplasma initans Wha1 precursor (wha1) and Wha2 precursor (wha2) genes, partial cds
4070	9084	14053	1.75	1.9E-02	P05081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4070	9084	14054	1.75	1.9E-02	P05081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4410	9400	14385	2.81	1.9E-02	AI452899.1	EST_HUMAN	l46d04_x1 Soares_NSF_F8_gW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
4852	7405	12623	3.15	1.9E-02	AL16150.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
344	5396	10403	1.36	1.8E-02	AW771104.1	EST_HUMAN	hn52c06_x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER29 repetitive element;
1142	8146	11178	1.42	1.8E-02	X17664.1	NT	H. francisci mRNA for myelin basic protein (MBP)
2607	7569	12684	1.45	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3138	8154		0.69	1.8E-02	AI805528.1	EST_HUMAN	1652a09_x1 Soares_NF1_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3'
3783	8786	13801	0.81	1.8E-02	AW879122.1	EST_HUMAN	MRI-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA

Page 50 of 209
Table 4
Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3763	8766	13802	0.81	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-004 OT0011 Homo sapiens cDNA
3970	8969		1.08	1.8E-02	AA861446.1	EST_HUMAN	ak24h04_s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1406935 3'
4306	9288	14284	1.59	1.8E-02	AW936363.1	EST_HUMAN	QV4-DT0021-301289-071-b11 DT0021 Homo sapiens cDNA
4788	9782	14765	0.95	1.8E-02	O60810	SWISSPROT	HYPOTHETICAL PROTEIN DJ845O24.2
895	5913	10852	1.21	1.7E-02	BE394869.1	EST_HUMAN	601310628F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'
1753	6747	11828	2.15	1.7E-02	AW573183.1	EST_HUMAN	601310628F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:29833740 3' similar to contains
1753	6747	11829	2.15	1.7E-02	AW573183.1	EST_HUMAN	hi34e03.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28333740 3' similar to contains
1833	6823		2.15	1.7E-02	AL169204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2054	7036		7.25	1.7E-02	AB004616.1	NT	Oryctolagus cuniculus mRNAs for mitosugulin29, complete cds
2569	7532		1.47	1.7E-02	78577495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
2929	7848	12866	1.08	1.7E-02	AI47616.1	EST_HUMAN	qb22a08_x1 Soares, pregnant uterus, NbHPU Homo sapiens cDNA clone IMAGE:16868882 3'
3433	8441		4.78	1.7E-02	AW827388.1	EST_HUMAN	hm45fd4_x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3016534 3' similar to contains
4045	8041		1.04	1.7E-02	AA868618.1	EST_HUMAN	MER19.61 MER19 repetitive element; ac194.s1 Strategene ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Aliu
4077	8071		1.88	1.7E-02	RO25061.1	EST_HUMAN	repetitive element; contains element MER24; repetitive element; ye86108.11 Soares fetal liver spleen 1NF1/S Homo sapiens cDNA clone IMAGE:124847 5'
4332	8323	14308	1.34	1.7E-02	AI305278.1	EST_HUMAN	qm03g01_x1 NCI_CGAP_Lu5_21 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X52359 ZNC
4396	9387	14370	1.47	1.7E-02	AW573183.1	EST_HUMAN	FINGER PROTEIN 30 (HUMAN);
4576	9564	14552	1.82	1.7E-02	Y00641.1	NT	hi34e03.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:29833740 3' similar to contains
4668	8653		6.38	1.7E-02	AI015076.1	EST_HUMAN	L1.11 L1 repetitive element;
507	5512		1.83	1.8E-02	AL021928.1	NT	Messenger RNA for anglerfish (Lophius americanus) somatostein 11
1816	6613	1680	1.13	1.6E-02	Y18886.1	NT	on51e02_s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1640858 3'
2187	7166	12285	1.01	1.6E-02	Q84173	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) ESTERASE-22
2187	7166	12286	1.01	1.6E-02	Q84176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) ESTERASE-22
2572	7635	12632	1.12	1.6E-02	AA484812.1	EST_HUMAN	ne1d06.61 NCI_CGAP_Ev1 Homo sapiens cDNA clone IMAGE:910687
2622	7584		0.85	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds
2851	7970	12887	0.73	1.6E-02	AF112282.1	NT	Lasea sp. isolate Ibd cytochrome oxidase III gene, partial cds; mitochondrial product
3447	8455	13481	5.11	1.6E-02	AW856852.1	EST_HUMAN	IL3-C10218-1602010-063-C07 CT0218 Homo sapiens cDNA

Page 51 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3758	8761	19761	1.1	1.8E-02	AL163301.2	NT	Human sapiens chromosome 21 segment HS21C101
4051	9047			1.82	1.6E-02	AF110520.1	Mus musculus major histocompatibility complex region NG27, NG28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RatGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
742	6765			23.96	1.5E-02	8923734	Human sapiens transcription factor (HSA150894), mRNA
2081	7062	12171	2.42	1.5E-02	N39521.1	EST_HUMAN	Yy27b07.81 Soares fetal liver spleen 1NF/S Homo sapiens cDNA clone IMAGE:243325.3'
2110	7090	12204	1.29	1.5E-02	AL161534.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
2887	8005	13017	1.24	1.5E-02	AJ006216.1	NT	Human sapiens CACNA1F gene, exons 1 to 48
2887	8005	13018	1.24	1.5E-02	AJ006216.1	NT	Human sapiens CACNA1F gene, exons 1 to 48
3641	8847	13654	0.88	1.5E-02	BF082942.1	EST_HUMAN	MR4-TN0115-080800-201-b12 TN0115 Homo sapiens cDNA
5006	8977	14952	0.97	1.5E-02	4503534	NT	Human sapiens eukaryotic translation initiation factor 4E (EIF4E) mRNA
414	5451			1.25	1.4E-02	AE002230.2	Chlamydophila pneumoniae AR39, section 58 of 94 of the complete genome
1101	6108	11138	3.65	1.4E-02	7705980	NT	Human sapiens NESH protein (LOC51225), mRNA
1237	6235		1.37	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1279	6278		2.38	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1486	6483		0.86	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAHH11.5'
2926	7945	12982	0.87	1.4E-02	7857040	NT	Human sapiens down-regulated in metastasis (DRM), mRNA
							Bifidobacterium longum Neu5H+ antipode (neuB), cyclic diaminase, and alpha-D-glactosidase (galD) genes, complete cds; and N-acetylglucosamine:N-acrose repressor protein (negCxyR) gene, partial cds
3140	8158	13177	2.22	1.4E-02	AF160969.2	NT	xb03d09_x1_NCI_LGAP_GJ1 Homo sapiens cDNA clone IMAGE:2575793.3'
3314	8325	13347	0.73	1.4E-02	AW074212.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3404	8413	13439	6.12	1.4E-02	AL161598.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3404	8413	13440	6.12	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3572	8579	13585	10.27	1.4E-02	8898919	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4361	9352	14331	7.08	1.4E-02	AW862088.1	EST_HUMAN	EST374761 MAGE resequences, MAGG Homo sapiens cDNA
4361	9352	14332	7.08	1.4E-02	AW962088.1	EST_HUMAN	EST374761 MAGE resequences, MAGG Homo sapiens cDNA
4726	9711	14695	6.63	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280.5'
4726	9711	14696	6.63	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280.5'
1828	6818		1.4	1.3E-02	BE739263.1	EST_HUMAN	601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335.5'
1815	6901	11884	1.7	1.3E-02	AL163201.2	NT	Human sapiens chromosome 21 segment HS21C001
2934	7853	12970	0.87	1.3E-02	MB1725.1	NT	Oenothera berlandiana NADH dehydrogenase subunit 2 (nad2) gene, exons 1-2
3141	8157	13178	1.9	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4288203.5'
3141	8157	13179	1.9	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4288203.5'
3862	8864		1.18	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds

Page 62 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4771	9755	14742		1.07	1.3E-02 U66081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV9S1P, TCRBV15S1, TCRBV11S1A1T, HVS rs ⁵ , TCRBV34S1, TCRBV14S1, TCRBV8S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBJ1S1, TCRBJ1S2,>Z65g01_r1 Soares retina NB24HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element;
353	5404	10414	4.04	1.2E-02 AA059989.1	EST_HUMAN	SWISSPROT	HYPOTHETICAL_17.1 KD PROTEIN IN PUR5 3REGION
450	5487	10502	1.62	1.2E-02 P08898	EST_HUMAN	qd86r12_x1 Soares testis_NH1 Homo sapiens cDNA clone IMAGE:1734870 3' similar to contains L1,H1 L1 repetitive element;	
729	5752	10773	5.89	1.2E-02 AI183522.1	EST_HUMAN	Hom sapiens chromosome 21 segment HS21C013	
2112	7092	12208	1.27	1.2E-02 AL163213.2	NT	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2116	7095	12209	1.07	1.2E-02 AV731704.1	EST_HUMAN	EST_HUMAN	X37609_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2375	7347	12488	1.15	1.2E-02 AW172350.1	EST_HUMAN	EST_HUMAN	X37609_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2564	7347	12488	1.16	1.2E-02 AW172350.1	EST_HUMAN	EST_HUMAN	ZmBBeg03_r1 Strategene ovarian cancer (R837219) Homo sapiens cDNA clone IMAGE:545020 5'
3028	8045		6.93	1.2E-02 AA075618.1	EST_HUMAN	EST_HUMAN	Y11608_s1 Soares placenta Nb24P Homo sapiens cDNA clone IMAGE:138903 3'
3215	8230	13261	1.97	1.2E-02 RG2805.1	EST_HUMAN	EST_HUMAN	Mus musculus interferon regulatory factor 5 (Irf5), mRNA
4729	8714	14698	0.85	1.2E-02 8754387	NT	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, R-Ret gene, and sodium phosphate transporter (NPT3) gene, complete cds
4761	9745	14731	3.66	1.2E-02 U91328.1	NT	NT	Cytochrome P450, part of CYP450, mRNA, partial cds
4876	9855		1.51	1.2E-02 AB019786.1	NT	NT	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
4912	9891	14865	2.45	1.2E-02 AV731704.1	EST_HUMAN	EST_HUMAN	Mus musculus POZ zinc finger transcription factor ODA-8 mRNA, complete cds
5025	9996	14969	1.29	1.2E-02 AF185576.1	NT	NT	ZmBBeg011_s1 Strategene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:530924 3'
1250	6243	11289	1.26	1.1E-02 AA010384.1	EST_HUMAN	EST_HUMAN	1q55b10_x1 NCI CGAP On23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW_XPF_HUMAN
1668	6684	11739	1.43	1.1E-02 X75491.1	NT	NT	H sapiens LIP A gene, exon 4
1668	6684	11740	1.43	1.1E-02 X75491.1	NT	NT	Q92886 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL;
1887	6972	12076	3.37	1.1E-02 BF345263.1	EST_HUMAN	EST_HUMAN	RC3-ST0197-120200-016-311 ST0197 Homo sapiens cDNA
2808	7828		4.07	1.1E-02 N98523.1	EST_HUMAN	EST_HUMAN	DKFZp586E0824_s1 588 (synonym: hule1) Homo sapiens cDNA clone DKFZp586E0824
3444	8452	13479	3.11	1.1E-02 A1653508.1	EST_HUMAN	EST_HUMAN	MR3-CT0173-111098-003-610 CT0176 Homo sapiens cDNA
3990	8988		0.69	1.1E-02 AW813798.1	EST_HUMAN	EST_HUMAN	Q92886 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL;
4683	9668	14650	2.3	1.1E-02 AL048383.2	EST_HUMAN	EST_HUMAN	RC3-ST0197-120200-016-311 ST0197 Homo sapiens cDNA
7	5087	10073	8.28	1.0E-02 AW848120.1	EST_HUMAN	EST_HUMAN	MR3-CT0173-111098-003-610 CT0176 Homo sapiens cDNA
2497	7465		0.85	1.0E-02 AA8086389.1	EST_HUMAN	EST_HUMAN	Q92886 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL;
3016	8033	15044	2.95	1.0E-02 BE835568.1	EST_HUMAN	EST_HUMAN	RC0-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA

Page 53 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3188	8204	13226	0.98	1.0E-02	BE968998.1	EST_HUMAN	601649867R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3943688 3'
4632	8617	146508	4.68	1.0E-02	8753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Crrt2), mRNA
4697	9582	146655	3.4	1.0E-02	R56567.1	EST_HUMAN	yg54h01.71 Soares fetal liver spleen 1NFLS_Homo sapiens cDNA clone IMAGE:1986833 6'
4855	8838	14810	1.72	1.0E-02	L05632.1	NT	Human glycoprotein hormone alpha-subunit (GCA) gene, 5' flank
8882	5800	10941	2.15	9.0E-03	A1798126.1	EST_HUMAN	wh42f09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element MER22 MER22 repetitive element ;
1245	6243			9.0E-03	BE781889.1	EST_HUMAN	60147242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2331	7305	12425	1.46	9.0E-03	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
4828	9812	14793	1.79	9.0E-03	BE047949.1	EST_HUMAN	I24481.0.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291468 5'
5026	8897	14970	1.02	9.0E-03	BE047949.1	EST_HUMAN	Mus musculus corticotropin releasing hormone receptor 2 (Crrt2), mRNA
498	6534		0.98	9.0E-03	6753521	NT	zh30e03.1 Soares_pineal_gland_N3HFG_Homo sapiens cDNA clone IMAGE:4135696 3' similar to contains element
974	6980	11023	52.19	2.78	8.0E-03	AA1723007.1	EST_HUMAN
2095	7076	12180	8.0E-03	AF1068585.1	NT	Hom sapiens adenylosuccinate lyase gene, complete cds	
3280	8282	13317	1.39	8.0E-03	AL163283.2	NT	Hom sapiens chromosome 21 segment 11S21C083
3581	8598	13603	0.68	8.0E-03	AJ131016.1	NT	Hom sapiens SCL gene locus
3591	8598	13604	1.23	8.0E-03	P328044	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4134	9129	14112	1.23	8.0E-03	P326444	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4258	9252	14239	0.95	8.0E-03	BE840419.1	EST_HUMAN	Q9V0-FN181-140700-30-910 FN0181 Homo sapiens cDNA
685	5709	10721	5.95	8.0E-03	BF383327.1	EST_HUMAN	CM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA
685	5709	10722	11.47	7.0E-03	AF0507183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
962	5977	11011	11.8	7.0E-03	AF0507183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1099	6108	11138	2.63	7.0E-03	AF731712.1	EST_HUMAN	AV731712 HTF_Homo sapiens cDNA clone HTFAZF10 5'
1372	6369	11418	2.08	7.0E-03	AA658298.1	EST_HUMAN	ab76b09.s1 Strategene fetal retina 837202 Homo sapiens cDNA clone IMAGE:853145 3'
1473	6470	11628	4.65	7.0E-03	AW303598.1	EST_HUMAN	xv1602.0.x1 Soares_NFL_T_GBC_S1_Homo sapiens cDNA clone IMAGE:281373 9 3'
2198	7765	12287	1.36	7.0E-03	P04299	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3680	8685	13687	0.92	7.0E-03	AW144463.1	EST_HUMAN	UH-B13-ekb-c-10-0-U_51_NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733681 3'
3722	8726	13726	0.78	7.0E-03	AF198344.1	NT	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4213	9208		1.05	7.0E-03	U60068.1	NT	Dicytostellum discoideum multidrug resistance transporter/Ser protease (tagC) mRNA, complete cds
4404	8395		1.12	7.0E-03	AW117711.1	EST_HUMAN	xs24f09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2605033 3' similar to TR:Q12887
4463	9458		1.1	7.0E-03	AW163088.1	EST_HUMAN	ACIDIC 82 kDa PROTEIN ; mhsa5s.y1 NCI_CGAP_G11 Homo sapiens cDNA clone IMAGE:29869836 5'

Page 54 of 209
Table 4

Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4830 9814			2.67	7.0E-03	AL168278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1221 6221	11263		8.46	6.0E-03	AW511148.1	EST_HUMAN	hg22a05_x1_Soares_NFL_T_GBC_S1_Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXK_HUMAN_O75469_ORPHAN NUCLEAR RECEPTOR PXR ;
1221 6221	11264		9.46	8.0E-03	AW511148.1	EST_HUMAN	hg22a05_x1_Soares_NFL_T_GBC_S1_Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXK_HUMAN_O75469_ORPHAN NUCLEAR RECEPTOR PXR ;
2689 7856	12770		1.02	6.0E-03	AF112374.1	NT	Danio rerio odorant receptor gene cluster
2820 7841	12857		4.18	6.0E-03	AA758135.1	EST_HUMAN	ah78611_s1_Soares_testis_NHT_Homo sapiens cDNA clone 1321772 3'
2820 7841	12858		4.18	6.0E-03	AA758135.1	EST_HUMAN	ah78611_s1_Soares_testis_NHT_Homo sapiens cDNA clone 1321772 3'
3173 8189			2.51	6.0E-03	H76589.1	EST_HUMAN	yr77h04_r1_Soares fetal liver spleen 1NFLS_Homo sapiens cDNA clone IMAGE:2113351 5'
3232 8247			0.85	6.0E-03	AF180338.1	NT	Notocampus sp. cyclochromis c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3298 8309	13335		1.31	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isocitin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3298 8309	13336		1.31	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isocitin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3470 8478			1.13	6.0E-03	W37985.1	EST_HUMAN	zz13a11.11_Soares_parathyroid tumor_NbHPA_Homo sapiens cDNA clone IMAGE:322172 5'
3576 8583	13588		6.07	6.0E-03	BF510986.1	EST_HUMAN	U1-H-B14-epm-n-c-06-0-U1.s1_NCI_CGAP_Sub8_Homo sapiens cDNA clone IMAGE:3087754 3'
3611 8618	13628		1.29	6.0E-03	BE077358.1	EST_HUMAN	RC1-B10605-26040-014-a07_BT0606_Homo sapiens cDNA
3690 8694	13698		1.18	6.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gpa1), mRNA
3850 8852			0.86	6.0E-03	BE250108.1	EST_HUMAN	600942804F1_NIH_MGC_15_Homo sapiens cDNA clone IMAGE:2989513 5'
4189 9192			1.31	6.0E-03	IN58946.1	EST_HUMAN	yy62zh_10_s1_Soares_multiple_sclerosis_2NbbHMSP_Homo sapiens cDNA clone IMAGE:278178 3'
4239 9233			1.27	6.0E-03	A1016833.1	EST_HUMAN	ov33c11_x1_Soares_testis_NHT_Homo sapiens cDNA clone IMAGE:1639124 3'
4556 9544	14629		6.94	6.0E-03	AA32422.1	EST_HUMAN	EST72116_Cerebellum II_Homo sapiens cDNA 5' end similar to EST containing Alu repeat
4950 9927			0.98	6.0E-03	L34170.1	NT	Human germline UBE2L1. Gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
661 5688	10696		1.81	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminocycl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
661 5688	10697		1.81	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminocycl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
662 5688	10696		2.2	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminocycl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
662 5688	10697		2.2	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminocycl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1095 6102	11132		1.24	5.0E-03	AJ010557.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase_RH3
2810 7572	12886		2.3	5.0E-03	AB033008.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds

Single Exon Probes Expressed in HBL100 C

Table 4
Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2619	7581	126892	2.52	4.0E-03	AJ277385.1	NT	Homo sapiens polyglutamine-containing C14orf4 gene
2624	7585	12695	1.04	4.0E-03	AL162284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3154	8170	13191	1.06	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151289-003-h08 HT0340 Homo sapiens cDNA
3154	8170	13192	1.06	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151289-003-h08 HT0340 Homo sapiens cDNA
3452	8460	13486	0.92	4.0E-03	AW18428.1	EST_HUMAN	x98f04_x1 NCI CGAP_Co18_Homo sapiens cDNA clone IMAGE:2865279 3'
3452	8460	13487	0.92	4.0E-03	AW18428.1	EST_HUMAN	x98f04_x1 NCI CGAP_Co18_Homo sapiens cDNA clone IMAGE:2865279 3'
3815	8548	13856	1.02	4.0E-03	Q13566	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3889	8889		1.73	4.0E-03	AJ0111712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
4480	9470	14451	1.08	4.0E-03	AJ732754.1	EST_HUMAN	ab18a08_x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
370	5419	10434	2.62	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
668	6886	10928	5.77	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1621	6618	11684	2.72	3.0E-03	AA468110.1	EST_HUMAN	nc73c05_s1 NCI CGAP_P22 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2231	7208		7.09	3.0E-03	Z32522.1	NT	S. cereale (cv. Hale) mRNA for triosephosphate isomerase
2232	7209	12323	0.92	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2232	7209	12324	0.92	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2923	7842		0.93	3.0E-03	Y08008.1	NT	Arribalzaga thailiana rpMt1 gene
3009	8026	13038	4.49	3.0E-03	BE37928.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:36068933 5'
3078	8094	13108	3.09	3.0E-03	AW802687.1	EST_HUMAN	IL2-UM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3333	8343	13361	2.08	3.0E-03	U34608.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3342	8351		2.09	3.0E-03	Y12500.1	NT	C.elegans sancdc gene
3870	8871	13876	7.05	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
3870	8871	13877	7.05	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
3925	8925	13915	1.8	3.0E-03	AV762392.1	EST_HUMAN	eh05f09_y5 Gieseler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4027	9023		1.04	3.0E-03	Z32521.1	NT	S. cereale (cv. Hale) mRNA for triosephosphate isomerase
4271	9264	14254	4.26	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4338	8329		0.69	3.0E-03	BE37928.1	EST_HUMAN	hf08g08_x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151934 3'
4387	8378	14359	5.15	3.0E-03	AL536141.1	EST_HUMAN	ab18a08_x5 P10 H3 cordon Homo sapiens cDNA 3'
4688	9871	14653	2.19	3.0E-03	AL732754.1	EST_HUMAN	ab18a08_x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
4705	9890	14673	6.19	3.0E-03	BE787845.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
4968	9845	14622	0.92	3.0E-03	4506414	NT	Homo sapiens RAP1_GTPase activating protein 1 (RAP1GA1) mRNA
4968	9845	14923	0.92	3.0E-03	4508414	NT	Homo sapiens RAP1_GTPase activating protein 1 (RAP1GA1) mRNA

Page 57 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5014	9985	14981	0.98	3.0E-03	S52213.1	NT	CD11b=leukocyte integrin alpha chain [human, Genomic, 104 nt, segment 23 of 31]
511	55448	10850	0.69	2.0E-03	Q04862	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
511	65448	10851	0.69	2.0E-03	Q04862	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
777	7731		10.87	2.0E-03	770874.1	EST_HUMAN	34156n03.1 Scores fetal liver spleen 1NF13 Homo sapiens cDNA clone IMAGE:1083415'
1348	63443	11394	1.92	2.0E-03	N20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1348	63445	11398	1.98	2.0E-03	AA661605.1	EST_HUMAN	nu8601.1s1 NCI CGAP At1 Homo sapiens cDNA clone IMAGE:1217593
1357	6354	11404	8.74	2.0E-03	AF284448.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1458	6455	11514	4.39	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAAN ANTIGEN 3 (PETA3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1485	6482	11537	1.7	2.0E-03		4557836 NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Elhers-Danlos syndrome type VI) (PL00) mRNA
1485	6482	11538	1.7	2.0E-03		4557836 NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Elhers-Danlos syndrome type VI) (PL00) mRNA
1556	6953		4.37	2.0E-03	P28400	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR
1734	6729	11808	1.18	2.0E-03	AA450138.1	EST_HUMAN	242a0.1 Scores total_fetus_N2HF8_9w Homo sapiens cDNA clone IMAGE:7891145'
1949	6935	12036	1.19	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2188	7167	12287	1.03	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2504	7472		3.15	2.0E-03	AW_37782.1	EST_HUMAN	U1-H-B11-adl-q-10-q-U1-s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:27170103'
3324	8342	13360	5.57	2.0E-03	AA450138.1	EST_HUMAN	242a0.1 Scores total_fetus_N2HF8_9w Homo sapiens cDNA clone IMAGE:7891145'
3338	6347	13385	0.86	2.0E-03	BF568895.1	EST_HUMAN	602183960711 NIH MGC 42 Homo sapiens cDNA clone IMAGE:43000703'
3582	8589	13593	5.61	2.0E-03	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IFFP2, LMF2, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
3997	8993	13680	2.35	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN (CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP56)
4099	9093		8.68	2.0E-03	U88491.1	NT	Rattus norvegicus 6-hydroxytryptamine receptor gene, partial cds
4303	9295		1.17	2.0E-03	AV287380.1	EST_HUMAN	U-H-BW0-air-q-0-0-U1-s1 NCI CGAP Sub6 Homo sapiens cDNA clone IMAGE:27304133'
4307	9299	14285	0.92	2.0E-03	AI064748.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4415	9405	14390	2.22	2.0E-03	L42512.1	NT	Drosophila melanogaster shortsighted class 2 (shs) mRNA, complete cds
4415	9405	14391	2.22	2.0E-03	L42512.1	NT	Drosophila melanogaster shortsighted class 2 (shs) mRNA, complete cds
4573	8981		1.9	2.0E-03	R87773.1	EST_HUMAN	yu45e02.91 Scores adult brain N2b41B55Y Homo sapiens cDNA clone IMAGE:1808903'
4861	8842	14814	0.94	2.0E-03	AF003528.1	NT	Homo sapiens X-linked amelodystrophic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
438	5474	10490	1.28	1.0E-03	H98471.1	EST_HUMAN	y98c08.11 Scores pineal gland_N3-IFG Homo sapiens cDNA clone IMAGE:2323345'
819	6639	10876	1.31	1.0E-03	AI720263.1	EST_HUMAN	est7008 x1 Barsteed colon HPI RB7 Homo sapiens cDNA clone IMAGE:23340593 similar to TRCQ1325 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE.;

Page 58 of 209
 Table 4
 Single Exon Probes Expressed In HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
819	5839	10877	1.31	1.0E-03	A1720263.1	EST_HUMAN	as70b08_x1_Bartered colon HPLB7_Homo sapiens cDNA clone IMAGE:2334039 3' similar to TRQ13825
1078	6085	11114	3.35	1.0E-03	A1865788.1	EST_HUMAN	Q13825_AJ-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
1098	6105	11135	1.17	1.0E-03	A1954572.1	EST_HUMAN	ww86a06_x1_NCI_CGAP_Pan1_Homo sapiens cDNA clone IMAGE:2422258 3'
1148	6152	11184	4.08	1.0E-03	A1692616.1	EST_HUMAN	ww86a01_x1_NCI_CGAP_Li24_Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element;
1977	6962	12069	2.86	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMWMI)
2093	7074	12168	4.54	1.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
2811	7830	12849	1.8	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1281 protein, partial cds
3118	8134	13153	2.17	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3118	8134	13154	2.17	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3228	8243	13285	0.75	1.0E-03	P05547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3466	8474	13498	0.78	1.0E-03	U68061.1	NT	Human MUC2 gene, promoter region
3466	8474	13499	0.76	1.0E-03	U68061.1	NT	Human MUC2 gene, promoter region
3681	8588	13840	1.51	1.0E-03	AB044400.1	NT	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
3831	8833	13840	0.76	1.0E-03	Z49849.1	NT	S.cerevisiae chromosome X reading frame ORF YJR149w
4312	9304	14288	5.29	1.0E-03	BE839182.1	EST_HUMAN	RC1-TN0128-160800-021-491 TN0128_Homo sapiens cDNA
4349	9340	14321	4.94	1.0E-03	BE24656.1	EST_HUMAN	TCBAP1D199 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBAP1D199
4528	9518	14505	0.91	1.0E-03	U29449.1	NT	sapiens cDNA clone TCBAP1D199
4677	9662	14644	1.69	1.0E-03	A1073485.1	EST_HUMAN	Ctenophoridium elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4677	9662	14645	1.69	1.0E-03	A1073485.1	EST_HUMAN	ov48c04_x1_Soares, testis_NHT_Homo sapiens cDNA clone IMAGE:1640282 3'
4678	9663	14884	5.57	1.0E-03	BE54087.1	EST_HUMAN	ov48c04_x1_Soares, testis_NHT_Homo sapiens cDNA clone IMAGE:1640282 3'
4605	9884	14885	8.4	1.0E-03	O46408	SWISSPROT	PM0-H10339-20040-010-D02_H10339_Homo sapiens cDNA
4896	9875	14843	1.32	9.0E-04	AA815400.1	EST_HUMAN	el61c12_s1_Soares, testis_NHT_Homo sapiens cDNA clone 1375318 3' similar to SW:AAATC_CHICK_P00504
4956	9956	14959	4.35	9.0E-04	P08547	SWISSPROT	ASPARTATE AMINO TRANSFERASE, CYTOPLASMIC;
4619	9604	14592	2.42	8.0E-04	U28185.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
2335	7309	12430	1.75	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2842	7602	12715	1.09	7.0E-04	AL163210.2	NT	Homo sapiens prion protein (PrP) gene, complete cds
3207	8222	13244	1.03	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXorf6) mRNA
3853	8855	13860	1.51	6.0E-04	A1862825.1	EST_HUMAN	wj15a11_x1_NCI_CGAP_Kid12_Homo sapiens cDNA clone IMAGE:2402876 3'

Page 59 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4060	8054	14041	3.01	6.0E-04	U45983.1	NT	Homo sapiens GCRB channikine receptor (CMKBR8) gene, complete cds
643	6971	10975	10.72	6.0E-04	O10341	SWISSPROT	HYPOTHETICAL 29.3 KD PROTEIN (ORF92)
1472	6469		1.4	5.0E-04	AW851844.1	EST_HUMAN	nk27e11.s1 NCL CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element
3329	8339	13367	1.21	5.0E-04	AA548933.1	EST_HUMAN	Haemophilus influenzae Rd section 63 of 163 of the complete genome
665	5891	10700	1.07	4.0E-04	U32748.1	NT	es70b08.x1 Barsteed colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
837	5856	10896	1.34	4.0E-04	AI720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOVYL-COA HYDRATASE; es70b08.x1 Barsteed colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
837	5856	10897	1.34	4.0E-04	AI720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOVYL-COA HYDRATASE; es70b08.x1 Barsteed colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1437	8434	11491	2.18	4.0E-04	AW765336.1	EST_HUMAN	RC3-C10254-130100-023-101 C10254 Homo sapiens cDNA
2030	7013	12122	1.19	4.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
2075	7057		0.94	4.0E-04	AL046704.1	EST_HUMAN	DKFZp434D059_r1_434 (synonym: hesc3) Homo sapiens cDNA clone DKFZp434D059 5'
2654	7519	12636	2.01	4.0E-04	DKFZp434D059	SWISSPROT	SERICIN-2 (SILK GUM PROTEIN 2)
3091	8107	13123	3.3	4.0E-04	AF281074.1	NT	Homo sapiens neutrophil 2 (NRP2) gene, complete cds, alternatively spliced
3776	8779		1.12	4.0E-04	AL163297.2	NT	Homo sapiens chromosome 21 segment HS21C067
4186	9189	14169	2.79	4.0E-04	AA576331.1	EST_HUMAN	HH10810_s1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4196	9189	14170	2.78	4.0E-04	AA576331.1	EST_HUMAN	HH10810_s1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4407	8388	14382	2.39	4.0E-04	AA086324.1	EST_HUMAN	Q361608_s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:3678910 5'
4915	9893	14867	3.42	4.0E-04	BE650680.1	EST_HUMAN	HH10810_s1 Scarses_multiple_sclerosis_2NhlMSP Homo sapiens cDNA clone IMAGE:279643 3' similar to HH10810_s1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL contains Alu repetitive element;
5019	8990	14985	1.02	4.0E-04	NA8313.1	EST_HUMAN	DKFZp761J221_r1_761 (synonym: hany2) Homo sapiens cDNA clone DKFZp761J221 5'
155	5221	10233	2.94	3.0E-04	AL119426.1	EST_HUMAN	180_KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
195	6259	10272	1.5	3.0E-04	P49259	SWISSPROT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
869	5887	10929	2.14	3.0E-04	U83991.1	NT	q228d03.y1 NCL CGAP Kidd11 Homo sapiens cDNA clone IMAGE:2028197 5'
1803	6784	11884	1.69	3.0E-04	AI26210.1	EST_HUMAN	q228d03.y1 NCL CGAP_Pi28 Homo sapiens cDNA clone IMAGE:21190823
1817	8807		2.03	3.0E-04	AI3598674.1	EST_HUMAN	1q23a02.x1 NCL CGAP_Pi28 Homo sapiens cDNA clone IMAGE:21190823
3236	8250	13271	4.06	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR (GDH)
3857	8859	13865	3.31	3.0E-04	P19448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
3942	8940		1.31	3.0E-04	A1271735.1	NT	Homo sapiens Xo pseudooxotonal region; segment 1/2
3976	8974		1.09	3.0E-04	BE140809.1	EST_HUMAN	RC04T1004-310599-028 HT0014 Homo sapiens cDNA
4671	9856		5.1	3.0E-04	BE153778.1	EST_HUMAN	PM0-HT0339-190200-007-912 HT0339 Homo sapiens cDNA

Page 60 of 209
 Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
175	6239	10250		1.52	2.0E-04	AF217796.1	NT
475	5511	10524		5.11	2.0E-04	AU146707.1	EST_HUMAN
896	5914	10953		6.36	2.0E-04	MB8524.1	NT
896	5914	10954		6.38	2.0E-04	MB8524.1	NT
1160	6164			3.63	2.0E-04	AU288021.1	EST_HUMAN
1187	6170			2.07	2.0E-04	AL163203.2	NT
1796	6187			0.97	2.0E-04	AE224268.1	NT
2120	7100			1.21	2.0E-04	AA478890.1	EST_HUMAN
2500	7488	12583		3.15	2.0E-04	U68061.1	NT
2818	7837	12934		1.18	2.0E-04	AI124529.1	EST_HUMAN
3226	8273	13298		1.1	2.0E-04	5174736	NT
3351	8360	13376		2.67	2.0E-04	BE02317.1	EST_HUMAN
3381	8389	13412		0.91	2.0E-04	U34374.1	NT
3818	8818	13825		1.04	2.0E-04	AW978441.1	EST_HUMAN
4020	9016			5.78	2.0E-04	U01029.1	NT
4534	8524	14511		1.51	2.0E-04	HE8265.1	EST_HUMAN
4634	8624	14512		1.51	2.0E-04	HF96265.1	EST_HUMAN
4651	8836			1.39	2.0E-04	U09226.1	NT
4891	9870	14838		1.87	2.0E-04	AB037897.1	NT
758	5779	10808		1.09	1.0E-04	H98346.1	EST_HUMAN
1058	6067	11087		1.86	1.0E-04	P11369	SWISSPROT ENDONUCLEASE
1097	6104	11133		3.05	1.0E-04	AW013847.1	EST_HUMAN
1097	6104	11134		3.05	1.0E-04	AW013847.1	EST_HUMAN
1342	6309			3.3	1.0E-04	U62918.1	NT

Page 61 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1568	6585	11646	3.97	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 68, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycaminidine synthase, and LAMP (LAMP) genes, complete cds
1598	6585	11647	3.97	1.0E-04	AF148806.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 68, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycaminidine synthase, and LAMP (LAMP) genes, complete cds
1824	68114	11908	1.7	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24;q14, microsatellite TKY38
3211	82226	13248	0.66	1.0E-04	Q82203	SWISSPROT	SPliceosome ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66) [Q81111.X] NCI CGAP_Gene Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
3651	88557	13983	0.72	1.0E-04	AI40282.1	EST_HUMAN	Mouse alpha 1 type-IV collagen mRNA
3948	89446	13936	1.86	1.0E-04	M140422.1	NT	AV347727 GLC Homo sapiens cDNA clone GL_GBB04 3'
3967	89666	13955	1.09	1.0E-04	AV647727.1	EST_HUMAN	Homino sapiens KIAA0237 gene product (KIAA0237), mRNA
4925	99022	14878	1.84	1.0E-04	7682015	NT	Homino sapiens KIAA0237 gene product (KIAA0237), mRNA
4925	99022	14878	1.64	1.0E-04	7682015	NT	Homino sapiens testis_NIH Homo sapiens cDNA clone 1292468 3'
639	57113	10727	1.84	9.0E-05	AA718833.1	EST_HUMAN	Pisum sativum mRNA for beta-1-3 glucanase (grn2 gene)
811	56332	10865	1.19	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1-3 glucanase (grn2 gene)
853	58722	1278	8.0E-05	AJ251646.1	NT	wf8a04_x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'	
4353	8344	14323	0.67	8.0E-05	AV044605.1	EST_HUMAN	RC3-CT0208-220989-011-E04 CT0208 Homo sapiens cDNA
345	5397	10404	11.8	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220989-011-E04 CT0208 Homo sapiens cDNA
345	5397	10405	11.8	7.0E-05	AW847445.1	EST_HUMAN	HUM072014F Human fovea cDNA clone EST_HFD072014
562	55956	10595	1.24	7.0E-05	LG9075.1	EST_HUMAN	HUM072014F Human fovea cDNA clone EST_HFD072014
562	55956	10596	1.24	7.0E-05	LG9075.1	EST_HUMAN	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
1038	6048	11078	1.43	7.0E-05	Q22949	SWISSPROT	Homo sapiens chromosome 21 segment HS21C078
2846	7606	12718	2.46	7.0E-05	AL163278.2	NT	Diclofenium discoidineum gene for TRFA, complete cds
3085	8101	13116	4.38	7.0E-05	AB009080.1	NT	Homo sapiens chromosome 21 segment HS21C001
3617	8624		1.24	7.0E-05	AI432413.1	EST_HUMAN	tg73cd9_x1 Scores_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2114416 3'
3943	8941		0.72	7.0E-05	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4247	9241	14225	1.61	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4769	8753	14741	0.66	7.0E-05	9845300	NT	Rat cytomegalovirus Mabstricht, complete genome
1976	6961	12067	1.6	8.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
1976	6961	12068	1.6	8.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA

Page 62 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2513	7481	12697	1.15	6.0E-05	A1655241.1	EST_HUMAN	WB54h06_x1 NC1 CGAP_GCB Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03250 DNA
2742	5696	10704	2.86	6.0E-05	AF053680.1	NT	TOPoisomerase I (HUMAN); Homo sapiens monocytic/ neutrophil elastase inhibitor gene, complete cds
1378	6376	11424	65.3	5.0E-05	AW392088.1	EST_HUMAN	QVA-ST0234-241189-040-h11 ST0234 Homo sapiens cDNA
1826	6816		2.39	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895). mRNA
2780	7811	12828	0.67	5.0E-05	AJ2510588.1	NT	Homo sapiens MEPA1 gene, promoter region and exon 1
3872	8873	13878	4.04	6.0E-05	AJ251842.1	NT	Homo sapiens partial SLC22A3 gene (or extraneuronal monoamine transporter (EMT), exon 1
2735	6289		3.87	4.0E-05	U12822.1	NT	Human renin (REN) gene, 5' flanking region
4355	9346	14325	0.92	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4355	9346	14326	0.92	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4725	9710		0.89	4.0E-05	AF164498.1	NT	Cryptosporidium parvum Isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
872	5697	10706	0.69	3.0E-05	A1248081.1	EST_HUMAN	q964c10_x1 Soares_fetal_liver_spleen_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
1042	6052	11082	1.01	3.0E-05	AW273851.1	EST_HUMAN	q964c10_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1114	6120	11148	1.64	3.0E-05	BF031898.1	EST_HUMAN	q964c10_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:38865142 5'
1114	6120	11149	1.84	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH MGc_86 Homo sapiens cDNA clone IMAGE:38865142 5'
2848	7608	12720	0.82	3.0E-05	Q62234	SWISSPROT	SKELEMIN
4257	9251	14237	9.42	3.0E-05	BE16921.1	EST_HUMAN	PM1-HT0521-120200-001-q10 HT0521_Homo sapiens cDNA
4257	9251	14238	9.42	3.0E-05	BE16921.1	EST_HUMAN	PM1-HT0521-120200-001-q10 HT0521_Homo sapiens cDNA
4342	9333	14316	0.94	3.0E-05	AA368879.1	EST_HUMAN	EST78996 Placenta (Homo sapiens) cDNA similar to similar to p53-associated protein
4342	9333	14317	0.94	3.0E-05	AA368879.1	EST_HUMAN	EST78996 Placenta (Homo sapiens) cDNA similar to similar to p53-associated protein
4486	9476	14456	0.76	3.0E-06	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4695	9680	14683	0.93	3.0E-05	AU125721.1	EST_HUMAN	AU125721_NT2RM4 Homo sapiens cDNA clone NT2RM402075 5'
2262	7239	12356	1.33	2.0E-05	AI286021.1	EST_HUMAN	q9861_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3_b2 MER3 repetitive element;
2606	7474	12689	1.85	2.0E-05	M13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds
2641	7601		5.26	2.0E-05	AA160582.1	EST_HUMAN	zq46a12_r1 Strategene hNT_neuron (RS37233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element;
3064	8081	13085	1.66	2.0E-05	BE066036.1	EST_HUMAN	RC3-BT0318-120200-014-h08 BT0319 Homo sapiens cDNA
3272	8284	13307	0.85	2.0E-05	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3287	8298	13325	1.06	2.0E-05	X89211.1	NT	H.sapiens DNA for endogenous retrovirus like element
3414	8423		0.69	2.0E-05	X95465.1	NT	S.cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
2623	7777	12694	1.86	1.0E-05	AL163822.2	NT	Homo sapiens chromosome 21 segment HS21C082
3565	8572	13578	2.01	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lantio 120 Suppressor of Hairy (Su(H)) gene, partial cds

Page 63 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3723	8727			1.18	1.0E-05 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3860	8892	139867		10.08	1.0E-05 PB1274	SWISSPROT	MOSAIC PROTEIN_LGN
4049	9045	140333		1.04	1.0E-05 AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4165	9150	14152		1.78	1.0E-05 AA31119.1	EST_HUMAN	ZW5904.1_Scar es testis_Nt Homo sapiens cDNA clone IMAGE:781494 5'
4703	9688	14671		1.9	1.0E-05 AW419134.1	EST_HUMAN	Xy9811.x1 NCI CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:285548 3'
2601	7563	12681		2.89	9.0E-06 AI583811.1	EST_HUMAN	W73608.x1 NCI CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3'
3022	8039	13048		4.56	9.0E-06 AI218983.1	EST_HUMAN	cg911b08.x1 Seares_placenta_8tc9weeks_21bbHP8tc9W Homo sapiens cDNA clone IMAGE:1759191 3'
3529	8535			2.64	9.0E-06 M61755.1	NT	Human sialin/glycosylate amine transferase (AGXT) gene, exons 1 and 2
2458	7771	12543		1.52	8.0E-06 AW362539.1	EST_HUMAN	RC3-CT0283-201198-011-h11 C1 0283 Homo sapiens cDNA clone IMAGE:8544251 3' similar to contains ab9010.1.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:8544251 3' similar to contains
984	5979			1.3	7.0E-06 AA669729.1	EST_HUMAN	IMR20.11 MER20 repetitive element;
1412	8410	11469		2.42	7.0E-06	7662177 NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2802	7822			6.96	7.0E-06 AI368252.1	EST_HUMAN	qw16g19.x1 NCI CGAP_U3S Homo sapiens cDNA clone IMAGE:18911296 3' similar to contains Aliu repetitive element;
2847	7867	12883		1.16	6.0E-06 BE069189.1	EST_HUMAN	QV3-BT0378-010300-105-d11 BT0378 Homo sapiens cDNA
2871	7890	12912		1.03	6.0E-06 QD1456	SWISSPROT	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
3609	8816	13925		0.93	6.0E-06 BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4609	7890	12912		1.96	6.0E-06 QD1456	SWISSPROT	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4616	9801	14557		2.14	6.0E-06 AI040099.1	EST_HUMAN	ox08e02.x1 Seares_fetal_liver_spleen_1NF1S_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element;
639	5667	10670		5.76	4.0E-06 R16287.1	EST_HUMAN	ya88c03.r1 Seares_infant_brain_NIB Homo sapiens cDNA clone IMAGE:532545 5' similar to contains Aliu repetitive element;contains L1 repetitive element;
836	5855	10895		6.98	4.0E-06 AW1023354.1	EST_HUMAN	xc89g12.x1 NCI CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Aliu repetitive element;contains element MER21 repetitive element;
1314	6311	11399		3.35	4.0E-06 AI334928.1	EST_HUMAN	1b33e09.x1 NCI CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1314	6311	11360		3.35	4.0E-06 AI334928.1	EST_HUMAN	1b33e09.x1 NCI CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1445	6442	11600		1.85	4.0E-06 BF365812.1	EST_HUMAN	QV2-NT0046-20080-250-07 NT0046 Homo sapiens cDNA
2203	7181	12304		1.59	4.0E-06 AW015401.1	EST_HUMAN	U-H-B10-est-f-05-0-U1.s1 NCI CGAP_Sub1 Homo sapiens cDNA, complete cds
2860	8008	13021		0.74	4.0E-06 AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3769	8802	13807		1.07	4.0E-06 AW848295.1	EST_HUMAN	IL3-CT0214-16200-074-B03 CT0214 Homo sapiens cDNA
4663	8848	14635		1.95	4.0E-06 AI886639.1	EST_HUMAN	wh94c10.x1 NCI CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element;

Page 64 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							Top Hit	Top Hit
5047	10018	14987	1.04	4.0E-08	AW817268.1	EST_HUMAN	QVO-ST0247-090200-105-e-005_ST0247_Homo_sapiens_cDNA	
2099	7080	12194	1.29	3.0E-06	AA700562.1	EST_HUMAN	z34b08.s1_Soares_fetal_liver_spleen_1NF1S_S1_Homo_sapiens_cDNA_clone IMAGE:432663 3' similar to contains L1_11 L1 repetitive element;	
2099	7080	12195	1.29	3.0E-08	AA700562.1	EST_HUMAN	z34b08.s1_Soares_fetal_liver_spleen_1NF1S_S1_Homo_sapiens_cDNA_clone IMAGE:432663 3' similar to contains L1_11 L1 repetitive element;	
2205	7182		1.18	3.0E-08	AF202635.1	NT	Homo sapiens PPP1200 mRNA, complete cds	
2851	7871	12886	1.09	3.0E-06	AA868218.1	EST_HUMAN	bkB911.s1_Soares_testis_NHT_Homo_sapiens_cDNA_clone IMAGE:1409252 3' similar to contains LTR1.13 L1_11 L1 repetitive element;	
3191	8207		2.25	3.0E-06	AB185777.1	EST_HUMAN	Wt22ef3.x1_NCL_CGAP_UT1_Homo_sapiens_cDNA_clone IMAGE:2425618 3' similar to TR:060734_060734 LINE1_LIKE PROTEIN :contains L1_12 L1 repetitive element;	
3695	8659	13701	1.73	3.0E-06	BE047094.1	EST_HUMAN	hq64412.x1_NCL_CGAP_HN13_Homo_sapiens_cDNA_clone IMAGE:3124151 3'	
3695	8659	13702	1.73	3.0E-06	BE047094.1	EST_HUMAN	hq84412.x1_NCL_CGAP_HN13_Homo_sapiens_cDNA_clone IMAGE:3124151 3'	
4430	8420	14406	2.51	3.0E-06	XS4816.1	NT	Homo sapiens gene for epsilon-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)	
4768	9750	14738	0.85	3.0E-06	JO4038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds	
4768	9750	14739	0.85	3.0E-06	JO4038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds	
202	5286		2.38	2.0E-06	PS54368	SWISSPROT	HOMEobox protein GOOSECOID	
1535	6533		4.34	2.0E-06	PI2144	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]	
2315	7280	12411	3.21	2.0E-06	AI677138.1	EST_HUMAN	wa4e03.x1_NCL_CGAP_Kid11_Homo_sapiens_cDNA_clone IMAGE:22970658 3' similar to contains MER30.b1 MER30 repetitive element;	
2397	7398	12489	1.48	2.0E-06	PD04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR	
2494	7462	12577	4.19	2.0E-06	PO6719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)	
3441	8449	13475	1.07	2.0E-06	AV687555.1	EST_HUMAN	AV657555.GLC_Homo_sapiens_cDNA_clone GLCFD05.3'	
3676	8681	13684	1.7	2.0E-06	AA137518.1	EST_HUMAN	zp02605.r1 Strategen ovarian cancer (#337219) Homo sapiens cDNA clone IMAGE:595232 5'	
3689	8693	13685	1.8	2.0E-06	AB003898.1	NT	Mus musculus gene for adrenor receptor A16, complete cds	
34	5114	10100	1.11	1.0E-06	O786082	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)	
649	5677	10684	1.24	1.0E-06	AF084364.1	NT	Mus musculus D6Mm5E protein (D6Mm5E) mRNA, complete cds	
1425	6422	11481	1.63	1.0E-06	PO9125	SWISSPROT	MEROZOITE PROTEIN CMz-8	
1491	6489	11644	0.92	1.0E-06	AL1632178.2	NT	Homo sapiens chromosome 21 segment HS21.C078	
1848	6934	12034	3.32	1.0E-06	AF104614.1	NT	Homo sapiens P47-phox (NCF1) gene, complete cds	
1948	6934	12035	3.32	1.0E-06	AF104614.1	NT	Homo sapiens P47-phox (NCF1) gene, complete cds	
4244	9238	14221	13.85	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8504 Met protein (M8504 Met gene, complete cds)	

Single Exon Probes Expressed in HBL105 Cells									
Probe Seq ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor		
							HS21C085		
4833	8910	14887	1.24	1.0E-06	AL1632885.2	NT	Homo sapiens chromosome 21 segment HS21C085		
4833	8910	14888	1.24	1.0E-06	AL1632885.2	NT	Homo sapiens chromosome 21 segment HS21C085		
4833	8910	14888	1.24	1.0E-06	AF003629.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions		
3559	6409	10421	1.02	9.0E-07	AF003629.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions		
3559	6409	10422	1.02	9.0E-07	AF003629.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions		
3559	6409	10422	1.02	9.0E-07	AF003629.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions		
4825	9810	14598	5.07	8.0E-07	AI288598.1	EST_HUMAN	q1B2g07_X1 Scores NihMPU_S1 Homo sapiens cDNA clone IMAGE:1878876 3'		
4825	9810	14599	5.07	8.0E-07	AI288598.1	EST_HUMAN	q1B2g07_X1 Scores NihMPU_S1 Homo sapiens cDNA clone IMAGE:1878876 3'		
4825	9810	14599	5.07	8.0E-07	AI288598.1	EST_HUMAN	CM3-C70277-221099-024-e11 CT0277 Homo sapiens cDNA		
1868	6857	11945	2.73	6.0E-07	AW855558.1	EST_HUMAN	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, heclease (SK12W), RD, complement factor B (B), and complement component C2 (C2) genes?		
2421	7392	12513	2.45	6.0E-07	AF019413.1	NT	SWISSPROT HYPOTHEtical 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION		
3895	8867	1.89	6.0E-07	PA41479	EST_HUMAN	wh84f012_X1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:23886547 3'			
324	6378	0.9	5.0E-07	AI831883.1	EST_HUMAN	EST83615 SupT cells Homo sapiens cDNA 5' end			
1040	6050	1.83	5.0E-07	AA380830.1	EST_HUMAN	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds			
4511	8501	14480	1.28	5.0E-07	AF49774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds		
3893	8893	13982	1.88	4.0E-07	AW008602.1	EST_HUMAN	ws84h05_X1 NCI CGAP_Co3 Homo sapiens cDNA clone IMAGE:25604697 3'		
438	5476	10492	5.45	3.0E-07	U19718.1	NT	Human microfibril-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons		
578	5810	10609	2.79	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 112		
1356	6353	11403	1.32	3.0E-07	MR9149.1	NT	Human polymorphic microsatellite DNA		
1586	6583	12320	0.94	3.0E-07	MR9149.1	NT	Human polymorphic microsatellite DNA		
2224	7201	12491	26.28	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0116-020300-001-111 BN0115 Homo sapiens cDNA		
2399	7370	12492	26.28	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0116-020300-001-111 BN0115 Homo sapiens cDNA		
2399	7370	12493	26.28	3.0E-07	BE005077.1	EST_HUMAN	Yd50f12_X1 Seaford fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:111695 5'		
2864	7982	12998	0.85	3.0E-07	U18704.1	EST_HUMAN	HYPOTHEtical 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR		
3086	8102	13117	1.84	3.0E-07	P28759	EST_HUMAN	EST850201 GLC Homo sapiens cDNA clone IMAGE:25604697 3'		
4537	8575	14566	8.16	3.0E-07	AY1650201.1	EST_HUMAN	EST_HUMAN		
4895	8874	14841	1.8	3.0E-07	T17850.1	EST_HUMAN	yc14h08_X1 Stratagen lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to		
4895	8874	14842	1.8	3.0E-07	T17850.1	EST_HUMAN	yc14h08_X1 Stratagen lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to		
4895	8874	10094	2.94	2.0E-07	AF262988.1	NT	gb:MR82882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)		
29	6109	10231	23.84	2.0E-07	L77669.1	NT	gb:MR82882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)		
153	5219	10232	23.84	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end		
153	5219	10233	23.84	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end		
181	6244	10265	129.68	2.0E-07	LJ38849.1	NT	Fugu rubripes beta-cytoplasmic (vascular) actin gene, complete cds		

Page 66 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (T _{op}) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
739	5762	10785	1.46	2.0E-07	AF00530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
739	5762	10786	1.46	2.0E-07	AF00530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
928	5946	10890	1.89	2.0E-07	AA223260.1	EST_HUMAN	z08b07_s1 Strategene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gb: J31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element;
930	5947	10981	1.68	2.0E-07	T63042.1	EST_HUMAN	yc15g04_s1 Strategene lung (F837210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element;
1145	6149	11181	0.83	2.0E-07	Q28768	SWISSPROT	16 AUTOANTIGEN
1565	6562	11625	2.13	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3804	8811	13619	20.05	2.0E-07	AF25348.1	NT	Homo sapiens cavedlin 1 (CAV1) gene, exon 3 and partial cds
1085	6092	11643	1.43	1.0E-07	AL163222.2	NT	Homo sapiens chromosome 21 segment HS21C082
2754	6488	11643	2.14	1.0E-07	P09256	SWISSPROT	GLYCOPROTEIN GPV
3869	6092		3.91	1.0E-07	AL163222.2	NT	Homo sapiens chromosome 21 segment HS21C082
4169	9164	14150	2.86	1.0E-07	AV718632.1	EST_HUMAN	AV718632 GLC C Homo sapiens cDNA clone GLCFNF04 5'
4169	9164	14151	2.86	1.0E-07	AV718632.1	EST_HUMAN	AV718632 GLC C Homo sapiens cDNA clone IMAGE:363026 5'
4973	8949	14927	1.22	1.0E-07	AA019181.1	EST_HUMAN	2e56g02_r1 Soares retina N2p4HR Homo sapiens cDNA clone IMAGE:2328273 3'
604	7725		2.23	8.0E-08	AI811352.1	EST_HUMAN	wd16b05_x1 Soares NFL_T_GBC_S11 Homo sapiens cDNA clone IMAGE:3943876 5'
1033	6043		0.8	8.0E-08	BE785469.1	EST_HUMAN	601580133F1_NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943876 5'
3468	8476		1.7	8.0E-08	BE785469.1	EST_HUMAN	601580133F1_NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943876 5'
79	5156	10167	3.2	7.0E-08	CD2357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1344	6341	11392	42.98	7.0E-08	X04809.1	NT	Rat mRNA for ribosomal protein L31
3495	8503	13617	0.7	7.0E-08	P15305	SWISSPROT	Dynein Heavy Chain (DyHC)
3495	8503	13618	0.7	7.0E-08	P15305	SWISSPROT	Dynein Heavy Chain (DyHC)
807	5828	10858	2.78	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
807	5828	10859	2.78	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2302	7277	12397	3.8	6.0E-08	BE144398.1	EST_HUMAN	MR0-HT0168-191189-004-q09 HT0168 Homo sapiens cDNA
2988	8906	13019	2.09	6.0E-08	7662473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4126	8121	14108	0.92	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
83	6160	10171	2.15	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2174	7153	12273	1.68	5.0E-08	AA493951.1	EST_HUMAN	nm03688_s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943183 similar to contains Alu repetitive element;
1722	8717	11783	1.2	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLID PROTEIN PRECURSOR
2815	7835		1.1	4.0E-08	AL079881.1	EST_HUMAN	DORSAL-VENTRAL PATTERNING TOLLID PROTEIN PRECURSOR DKFZp434.01428_r1 434 (synonym: libes3) Homo sapiens cDNA clone DKFZp434.01428 5'

Page 67 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
206	5270		8.87	2.0E-08	AW302868.1	EST_HUMAN	nr87106.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767739' 3'
227	5290			7.99	2.0E-08 AA425598.1	EST_HUMAN	zw48f07.r1 Seares_bb1_fetus_Nb2hF8_Bw Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER15 repetitive element;
493	5529	10637		2.63	2.0E-08 AF498349.1	NT	Galius galius Dach2 protein (Dach2) mRNA, complete cds
652	5680	10686	9.13	2.0E-08 AW886438.1	EST_HUMAN	MF0-010080-240200-001-008 O10080 Homo sapiens cDNA	
652	6690	10687	9.13	2.0E-08 AW886438.1	EST_HUMAN	MF0-0080-240200-001-008 O10080 Homo sapiens cDNA	
875	5891		26.56	2.0E-08 BE280477.1	EST_HUMAN	601155321F NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'	
1323	6321	11369	1.74	2.0E-08 AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047	
1702	6697		1.75	2.0E-08 BE734871.1	EST_HUMAN	601570483F NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845199' 5'	
1818	6808		3.33	2.0E-08 AW270271.1	EST_HUMAN	xp43f11.x1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:2743149' 3'	
2352	7326	12443	1.22	2.0E-08 AA731948.1	EST_HUMAN	nw64h01.st NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1251409 3' similar to contains L1.13 L1 repetitive element;	
2472	7441		1.31	2.0E-08 K00216.1	NT	Sheep His-1RNA-GUG	
3135	8151	13173	6.15	2.0E-08 O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR	
3135	8151	13174	6.15	2.0E-08 O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR	
3769	8772		1.61	2.0E-08 AW813620.1	EST_HUMAN	RC3-ST0197-161099-012403 ST0197 Homo sapiens cDNA	
4281	9274		1.32	2.0E-08 AA459040.1	EST_HUMAN	aa26c07.11 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element;	
4800	9784		3.44	2.0E-08 AW572881.1	EST_HUMAN	he17h03.22 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918327 3' similar to contains Ali repetitive element;	
1738	8733	11810	1.28	1.0E-08 AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds	
1898	6981		1.58	1.0E-08 BE141959.1	EST_HUMAN	PM2-HT0130-150898-001-f12 HT0130 Homo sapiens cDNA	
3119	8135	13155	1.06	1.0E-08 BE246844.1	EST_HUMAN	TCBAP1DS232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBAP1 Homo sapiens cDNA clone TCBAP1DS232	
3119	8135	13156	1.06	1.0E-08 BE246844.1	EST_HUMAN	TCBAP1DS232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBAP1 Homo sapiens cDNA clone TCBAP1DS232	
4120	9114	14100	3.28	9.0E-09 AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079	
4120	9114	14101	3.28	9.0E-09 AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079	
3526	8532		1.62	7.0E-09 D88842.1	NT	Homo sapiens DNA for 3-ketothiacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3	
4310	9302	14287	1.19	6.0E-09 AF111197.2	EST_HUMAN	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene	
4821	9805	14787	4.89	6.0E-09 BE159421.1	EST_HUMAN	PM4-HT0521-160200-001-h05 HT0521 Homo sapiens cDNA	
1390	6387	11439	2.89	5.0E-09 BE119284.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA	

Page 69 of 209
Table 4
1. Human Proteins Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							Top Hit Descriptor	Top Hit Descriptor
146	5212	10228	11.08	8.0E-10	U63630_2	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds	
4078	8072	14059	1.87	8.0E-10	AA376832_1	EST_HUMAN	EST89564 Small intestine 1 Homo sapiens cDNA 5' end	
692	5716	10732	39.41	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LC551588), mRNA	
692	5716	10733	39.41	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LC551588), mRNA	
1583	65680	11643	1.69	7.0E-10	Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)	
2488	7456		9.17	7.0E-10	POB547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	
3014	8031	13041	2.59	7.0E-10	X00856_1	NT	H. sapiens DHFR gene, exon 3	
902	5920	10856	2.89	6.0E-10	AJ400877_1	NT	Homo sapiens CGAP F728 Homo sapiens cDNA clone IMAGE:2085021 3'	
2608	7568	12683	1.11	6.0E-10	AI424406_1	EST_HUMAN	IT02d07_x1 NCI CGAP F728 Homo sapiens cDNA	
4598	9586		2.52	6.0E-10	AW853719_1	EST_HUMAN	RC3-CT0254-031058-01-812 CT0254-1 Homo sapiens cDNA	
761	5773		4.91	6.0E-10	AL06804_1	EST_HUMAN	DKFZp434N218_1_7_134 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N218_5	
3395	8403	13429	1.15	6.0E-10	QD01033	SWISSPROT	HYPOTHETICAL PROTEIN	
4833	9817	14785	1.25	5.0E-10	AF181897_1	NT	Homo sapiens WRN (WRN) gene, complete cds	
111	5183		1.48	4.0E-10	AI221083_1	EST_HUMAN	qp09109_x1 Soares_810weeks_2NbHP816eW Homo sapiens cDNA clone IMAGE:1798049 3'	
676	56008	10507	1.35	4.0E-10	AA515260_1	EST_HUMAN	similar to contains LTRB2b LTR8 repetitive element;	
1950	68336	12037	1.15	4.0E-10	AW594708_1	EST_HUMAN	nf844a01_s1 NCI CGAP C03 Homo sapiens cDNA clone IMAGE:924648 3'	
2489	7467	12552	3.14	4.0E-10	AL163303_2	NT	similar to contains LTRB2b LTR8 repetitive element;	
904	5921	10958	1.72	3.0E-10	IN36113_1	EST_HUMAN	yg52f06_s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:272853 3' similar to contains	
1333	6331		4.3	3.0E-10	AY005150_1	NT	yy52f06_s1 Soares melanocyte 2NbHM Homo sapiens cDNA precursor, gene, complete cds	
38	5116	10102	1.49	2.0E-10	P49888	SWISSPROT	L1.11 L1 repetitive element;	
38	5116	10103	1.49	2.0E-10	P49888	SWISSPROT	Hom sapiens extracellular glycoprotein lactitin precursor, gene, complete cds	
1857	6846		2.98	2.0E-10	U80017_1	EST_HUMAN	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)	
2917	7836		1.37	2.0E-10	BF670407_1	EST_HUMAN	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)	
1419	6476		1.01	1.0E-10	AV887767_1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCCA11_3'	
1570	6567	11628	2.18	1.0E-10	AV652123_1	EST_HUMAN	OVO-CT0225-191199-058-e018 CT0226 Homo sapiens cDNA	
2505	7473		2.43	1.0E-10	AV852001_1	EST_HUMAN	EST_HUMAN	
3420	8428	13454	0.59	1.0E-10	AW832812_1	EST_HUMAN	QV2-IT0003-161199-013-910 TT0003 Homo sapiens cDNA clone DKFZp434N1317_5'	
3462	8470		0.97	1.0E-10	AI041685_1	EST_HUMAN	DKFZp434N1317_1_134 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317_6'	
3754	8470		1.16	1.0E-10	AI041685_1	EST_HUMAN		

Page 70 of 209

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3908	8908	6.83	1.0E-10	AF213684.1	NT	<i>Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete cds</i>
4007	9003	13.890	4.83	1.0E-10	U52111.2	NT <i>Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CaMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein > protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CaMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein ></i>
4007	9003	13.981	4.83	1.0E-10	U52111.2	NT <i>Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds</i>
4013	9009	13.989	2.16	1.0E-10	AB031059.1	NT <i>Homo sapiens PCCX1 mRNA, last exon</i>
4046	9042	2.35	1.0E-10	M30629.1	NT <i>Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon</i>	
259	5318	10328	1.16	9.0E-11	BE145800.1	EST_HUMAN <i>DKFZp547D225_11_547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225_11_547</i>
2046	7028	12139	4.32	9.0E-11	AL134395.1	EST_HUMAN <i>DKFZp547D225_11_547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225_11_547</i>
2046	7028	12140	4.32	9.0E-11	AL134395.1	EST_HUMAN <i>DKFZp547D225_11_547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225_11_547</i>
3289	8310	13337	2.54	9.0E-11	AL134395.1	EST_HUMAN <i>DKFZp547D225_11_547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225_11_547</i>
3289	8310	13338	2.54	9.0E-11	AL134395.1	EST_HUMAN <i>DKFZp547D225_11_547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225_11_547</i>
4371	9363	14843	0.89	9.0E-11	AA1775985.1	EST_HUMAN <i>aa7801.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970287_3'</i>
3042	8059		8.11	8.0E-11	H19971.1	<i>yn53f1.s1 Soares adult brain N2b5fB557 Homo sapiens cDNA clone IMAGE:1721713_3' similar to contains L1 repetitive element;</i>
3930	8930	13921	4.2	8.0E-11	N23712.1	<i>EST_HUMAN y48606.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA 5' end</i>
1422	6419	11479	7.0E-11	AA1330642.1	EST_HUMAN <i>EST34392 Embryo, 6 week Homo sapiens cDNA 5' end</i>	
409	6448	10467	5.12	8.0E-11	M65270.1	NT <i>Human matrix Glc protein (MGP) gene, complete cds</i>
409	6448	10486	5.12	8.0E-11	M65270.1	NT <i>Human matrix Glc protein (MGP) gene, complete cds</i>
12	6092	10076	0.93	5.0E-11	AL163283.2	NT <i>Human sapiens chromosome 21 segment HS21C083</i>
3284	5092	10076	0.92	5.0E-11	AL163283.2	NT <i>SWISSPROT</i>
4107	9101	14088	1.53	5.0E-11	P48034	EST_HUMAN <i>ALDEHYDE OXIDASE</i>
1377	6374		5.75	4.0E-11	AA486042.1	EST_HUMAN <i>Soares testis NHT Homo sapiens cDNA clone IMAGE:3909285_5'</i>
2718	7875	12788	4.93	4.0E-11	BE885900.1	NT <i>Homo sapiens chromosome 21 segment HS21C047</i>
2800	7818	12840	1.26	4.0E-11	AL163247.2	NT <i>HUMSUP769 Human brain cDNA Homo sapiens cDNA clone IMAGE:730559_5'</i>
4485	8475	14455	0.75	4.0E-11	D44666.1	EST_HUMAN <i>Mus musculus expressed in non-metastatic cells 2, protein (MN23B) (Nme2), mRNA</i>
1486	8457	11616	18.61	3.0E-11	6879077	NT <i>wj36d06.x1 NCI CGAP Kid12 Homo sapiens cDNA clone IMAGE:2404811_3'</i>
2829	7849		0.81	3.0E-11	AL163833.1	EST_HUMAN <i>EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end</i>
4164	8149		1.05	3.0E-11	AA309248.1	EST_HUMAN <i>qj36c04.x1 Soares, testis NHT Homo sapiens cDNA clone IMAGE:1762102_3' similar to contains MER10_13</i>
945	5982	10985	1.02	2.0E-11	AI150502.1	EST_HUMAN <i>MER10 repetitive element;</i>

Page 71 of 209
Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1166 6169	11204		3.84	2.0E-11 R24807.1	EST_HUMAN	Yg43e12.11 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:35144 5'	
1166 6169	11205		3.84	2.0E-11 R24807.1	EST_HUMAN	Yg43e12.11 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:35144 5'	
1576	6573	11634	3.97	2.0E-11 L17432.1	NT	Gallus gallus rho-globin, beta-H globin, epsilon-globin, and olfactory receptor-like protein COR3beta (COR3beta) genes, complete cds	
1576	6573	11635	3.97	2.0E-11 L17432.1	NT	Gallus gallus rho-globin, beta-H globin, epsilon-globin, and olfactory receptor-like protein COR3beta (COR3beta) genes, complete cds	
2891	7649	12763	0.83	2.0E-11 AF026263	NT	Human endogenous retrovirus HERV-P-T47D	
3123	8139	13161	6.88	2.0E-11 P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPEPTIDE (VERSION 1)	
3251	8284	13285	0.74	2.0E-11 AI478617.1	EST_HUMAN	lnf54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161836 3'	
3417	8425		0.94	2.0E-11 AF020563.1	NT	Hom sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 6	
4321	9313		1.04	2.0E-11 BE086537.1	EST_HUMAN	RC3-BT0316-1/0200-014-605 BT0316 Homo sapiens cDNA HS21C027	
4474	9484		0.76	2.0E-11 AL163227.2	NT	Hom sapiens chromosome 21 segment HS21C027	
4779	9763		1.84	2.0E-11 BE062558.1	EST_HUMAN	QV2-BT0258-281098-014-011 BT0258 Homo sapiens cDNA	
6888	5693	10702	0.78	1.0E-11 AJ131018.1	NT	Hom sapiens SCL gene locus	
775	5797	10825	1.24	1.0E-11 AL163209.2	NT	Hom sapiens chromosome 21 segment HS21C009	
1198	6199	11235	2.84	1.0E-11 AL1632279.2	NT	Hom sapiens chromosome 21 segment HS21C078	
1469	6466		1.4	1.0E-11 AF119914.1	NT	Hom sapiens PRO3078 mRNA, complete cds	
1988	6971	12075	1.14	1.0E-11 P16258	SWISSPROT	OXYSTEROL-BINDING PROTEIN	
2067	7049	12157	2.2	1.0E-11 AF000573.1	NT	Hom sapiens homogenizable 1,2-di-oxygenase gene, complete cds	
3419	8427	13453	0.93	1.0E-11 BE004315.1	EST_HUMAN	CMD-BN0105-170300-282412 BN0105 Homo sapiens cDNA	
4528	9516	14502	1.42	7.0E-12 Q05904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)	
3471	8479		0.75	6.0E-12 AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF065	
4222	9216	14195	0.87	6.0E-12 AA732516.1	EST_HUMAN	nz88f11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alt repetitive element:	
5074	10043	15009	1.48	6.0E-12 M22486.1	NT	Human chromosomes 21 distal long arm DNA	
1026	6038	11088	2.25	5.0E-12 T08573.1	EST_HUMAN	EST04462 Fatal brain, Streptococcus (Cat#362026) Homo sapiens cDNA clone HFBDV33	
3306	8317	13343	1.16	5.0E-12 BE04778.1	NT	Hom sapiens Xq pseudautosomal region, segment 2/2	
3644	8650	13656	7.07	5.0E-12 AJ271736.1	EST_HUMAN	lta22b15.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:460676 3'	
242	5303	10313	4.12	4.0E-12 AA700326.1	EST_HUMAN	274911.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'	
243	5303	10313	6.02	4.0E-12 AA700328.1	EST_HUMAN	274911.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TRQ13539 Q13639	
4487	9477	14457	0.7	4.0E-12 AI689984.1	EST_HUMAN	b26h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone MARINER TRANSPOSAE_1	

Page 72 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
612 5639	10641		3.43	3.0E-12 AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517	
612 5639	10642		3.43	3.0E-12 AW341683.1	EST_HUMAN	O14617 SMRP_;	
1613 6609	11673		1.82	2.0E-12 AWB02131.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517	
3388 8394	13418		0.75	2.0E-12 8754495	NT	IL6-UM0071-120400-085-a05 UM0071 Homo sapiens cDNA O14517 SMRP_;	
3998 8594	13591		0.85	2.0E-12 J01884.1	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2) mRNA	
3998 8594	13592		0.85	2.0E-12 J01884.1	NT	Rat U3A small nuclear RNA	
3998 8594	13592		0.85	2.0E-12 J01884.1	NT	Rat U3A small nuclear RNA	
3998 8594	13592		0.85	2.0E-12 J01884.1	NT	CMD-BT0281-01 311B9-087-4C3 BT0281 Homo sapiens cDNA	
4287 9289	14712		2.34	2.0E-12 BE068509.1	EST_HUMAN	CM0-BT0281-01 311B9-087-4C3 BT0281 Homo sapiens cDNA	
4742 9727	14713		1.72	2.0E-12 O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 16)	
4742 9727	14713		1.72	2.0E-12 O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 16)	
123 5192	10205		1.65	1.0E-12 AW627674.1	EST_HUMAN	hhr080.x1 NCI CGAP_GUT Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11	
1841 6927			1.12	1.0E-12 AIB71726.1	EST_HUMAN	lmer18 repetitive element; ywn51107.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2438493 3' similar to contains L1,b3 L1	
2897 8015	13027		1.34	1.0E-12 AF000891.1	NT	Hom sapiens testis-specific Testis Transcript Y 2 (TY2) mRNA, partial cds	
2897 8015	13027		1.34	1.0E-12 AF000891.1	NT	Hom sapiens testis-specific Testis Transcript Y 2 (TY2) mRNA, partial cds	
2897 8015	13028		1.34	1.0E-12 AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3-004070 5'	
3783 8786	13189		28.33	1.0E-12 AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3-004070 5'	
3783 8786	13190		28.33	1.0E-12 AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3-004070 5'	
3543 8550			1.53	9.0E-13 AJ271735.1	NT	Hom sapiens Xq pseudautosomal region; segment 1/12	
3843 8845	13854		0.85	9.0E-13 AB29800.1	NT	Hom sapiens CST gene for cerebroside sulfotransfere, exon 1, 2, 3, 4, 5	
707 5731	10747		4.84	8.0E-13 U28198.1	NT	Hom sapiens prion protein (PrP) gene, complete cds	
707 5731	10748		4.84	8.0E-13 U29185.1	NT	Hom sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds	
1802 6783	11883		2.36	8.0E-13 U80011.1	NT	Hom sapiens chromosome 21 segment HS21C007	
2044 7028	12137		3.41	8.0E-13 AL163207.2	EST_HUMAN	Y8204.r1 Soares placenta Nb2hIP Homo sapiens cDNA clone IMAGE:72B350 3' similar to contains Alu	
3248 8261			0.67	5.0E-13 R78338.1	EST_HUMAN	z177a12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:72B350 3' similar to contains element MER22 repetitive element;	
3313 8324			1.38	5.0E-13 AA435773.1	EST_HUMAN	repetitive element contains element MER22 repetitive element	
1830 6820			9.36	4.0E-13 AW378814.1	EST_HUMAN	PM2-HT0224-221089-001-e11 H10224 Homo sapiens cDNA	
2391 7382			1.32	4.0E-13 AF00529.1	NT	Hom sapiens glyican 3 (GPC3) gene, partial cds and flanking repeat regions	
4604 8592			1.02	4.0E-13 AA454054.1	EST_HUMAN	2A48d07.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:7B5469 5'	
179 6242			4.21	3.0E-13 AF003528.1	NT	Hom sapiens X-linked epidermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	

Page 73 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
854	6873		0.84	3.0E-13 AA430310.1	EST_HUMAN	ZN68908_r1_Soares testis NHT Homo sapiens cDNA clone IMAGE:7814085'		
2309	7284	12404	1.24	3.0E-13 AJ271738.1	NT	Homo sapiens Xq1 pseudautosomal region 21 segment HS2/C2010		
2408	7379		2.01	3.0E-13 AL165210.2	NT	Homo sapiens chromosome 21 segment HS2/C2010		
2593	7656	12870	3.02	3.0E-13 BT372962.1	EST_HUMAN	CMS3-F10100-140700-242-h08 F10100 Homo sapiens cDNA clone IMAGE:13240353'		
3113	8129		2.08	3.0E-13 AA745844.1	EST_HUMAN	obj8dd2_s1_NCI CGAP_kids Homo sapiens cDNA clone containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RP1.8a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >		
149	5215	10229	2.57	2.0E-13 U52111.2	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds		
237	52959	10310	0.88	2.0E-13 U23839.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds		
1251	6249	11290	6.43	2.0E-13 AF239710.1	NT	Homo sapiens F8_9W OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3'		
3208	82223	13245	1.32	2.0E-13 BF431899.1	EST_HUMAN	mbab76105_x1_Soares NSF_F8_9W OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3'		
3428	8436	13462	1.88	2.0E-13 AF108907.1	NT	Homo sapiens chromosome 21 segment HS2/C2078		
3992	8969		2.02	2.0E-13 AL16327B.2	NT	Homo sapiens fibroblast growth factor 1 (human, kidney, genomic), 342 nt, segment 2 of 2		
289	5346	10358	1.08	1.0E-13 S74128.1	NT	FGF-1=fibroblast growth factor 1 (human, kidney, genomic), 342 nt, segment 2 of 2		
877	5895	10836	4.81	1.0E-13 AJ007973.1	NT	Homo sapiens LGMDBB gene		
1316	6313	11362	1.45	1.0E-13 X87344.1	NT	Homo sapiens LGMDBB gene		
1972	6957	12062	1.73	1.0E-13 AA720574.1	EST_HUMAN	IPF2 and RING3, 9, 13 and 14		
4461	9451	14432	1.6	1.0E-13 BF340987.1	EST_HUMAN	H.sapiens DMA, DMB, HLA-Z1, IPP2, TAP1, LMP1, TAP2, DOB, DQB2 and RING3, 9, 13 and 14		
331	5383	10391	2.84	8.0E-14 AA781159.1	EST_HUMAN	H.sapiens DMA, DMB, HLA-Z1, IPP2, TAP1, LMP1, TAP2, DOB, DQB2 and RING3, 9, 13 and 14		
332	6384	10392	2.83	9.0E-14 AA781169.1	EST_HUMAN	IPF2 and RING3, 9, 13 and 14		
2427	7398		3.07	9.0E-14 AW861577.1	EST_HUMAN	H.sapiens DMA, DMB, HLA-Z1, IPP2, TAP1, LMP1, TAP2, DOB, DQB2 and RING3, 9, 13 and 14		
2680	7638	12753	3.39	9.0E-14 AB038162.1	NT	Homo sapiens TFF gene cluster for wif1 factor, complete cds		
3037	8054	13062	5.01	9.0E-14 AW5132986.1	NT	Sox5/h05_x1_NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2707833_3'		
3708	8712	13715	7.31	9.0E-14 D14547.1	NT	Human DNA, SINE repetitive element		
4612	9598	14584	1.69	9.0E-14 AJ002153.1	NT	Sequinus oedipus gene for seminal vesicle secreted protein semenogelin 1		
3418	8426		1.04	8.0E-14 BE463263.1	EST_HUMAN	h27169_x1_NCI CGAP_L024 Homo sapiens cDNA clone IMAGE:1447983_3'		
3849	8851		3.5	8.0E-14 R76299.1	EST_HUMAN	M72e03_r1_Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:1447983_3'		

Page 74 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1590	7751		2.98	7.0E-14	AW_151673.1	EST_HUMAN	x67e10.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623148 3' similar to contains MER10.12
366	6415	10428	13.89	8.0E-14	AF020603.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
814	5841	10844	4.27	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE PROTEIN) ASSOCIATED PROTEIN 2 (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
4886	9865	14836	1.45	5.0E-14	AW073791.1	EST_HUMAN	xp03b05.x1 NCI CGAP_Gui1 Homo sapiens cDNA clone IMAGE:2675185 3' similar to contains L1.L2.L1 repetitive element;
1108	7739		1.69	4.0E-14	PO4928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1839	6829	111818	5.27	4.0E-14	AJ007973.1	NT	Homo sapiens LGMD2B gene
3968	8671		0.88	4.0E-14	AA046502.1	EST_HUMAN	2k67a06.1r Soares, pregnant uterus_NbHu Homo sapiens cDNA clone IMAGE:279190 3' similar to y775c12.s1 Soares, multiple sclerosus_2NbHMSp Homo sapiens cDNA
4168	9163	14148	0.8	4.0E-14	N46328.1	EST_HUMAN	contains L1.L3.L1 repetitive element;
935	5952	10984	1.12	3.0E-14	X85486.1	NT	R, nonvegic mRNA for CP-622 protein
389	6427	10442	2.33	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
389	6427	10443	2.33	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
681	7727	10716	7.63	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2324	7288		1.24	2.0E-14	AW372888.1	EST_HUMAN	RC5-BT0577-091299-031-D12 B10377-Homo sapiens cDNA
2385	7368		1.08	2.0E-14	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
2455	7425	12539	1.41	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1050	6059	11088	1.59	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
1382	6379	11427	4.61	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1382	6379	11428	4.61	1.0E-14	AL163268.2	NT	Homo sapiens chromosome X region from flamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
1955	6941	12043	21.53	1.0E-14	L44140.1	NT	Homo sapiens chromosome 21 segment HS21C103
2121	7101	12213	4.33	1.0E-14	AL163303.2	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2343	7317	12437	18	1.0E-14	AF061689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2874	7893	12816	1.2	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3094	8110	13127	5.68	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-s09_1 CT0432 Homo sapiens cDNA
3094	8110	13128	6.88	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-s09_1 CT0432 Homo sapiens cDNA
3792	8175	13800	1.7	1.0E-14	AA682894.1	EST_HUMAN	aa8Bc12.s1 Stratogene schizo brain S11 Homo sapiens cDNA clone IMAGE:2750509 3'
4348	9359	14320	1.98	1.0E-14	AW275852.1	EST_HUMAN	xg39h10.x1 NCI CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2750509 3'
1541	6539		1.39	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPT), mRNA

Page 75 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							Homo sapiens transcription factor IgHm enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
2108	7088			1.04	9.0E-16 AF198779.1	NT	
2739	5513			1.02	8.0E-15 BE261482.1	EST_HUMAN	IMAGE:3164025' 5'
979	5894	11027		4.97	6.0E-15 AJ2/11736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
407	5444	10484		4.86	5.0E-15 AL163208.2	NT	Homo sapiens chromosome 21; segment HS21C008
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H2A-H) gene, R-Ret gene, and sodium phosphate transporter (NP73) gene, complete cds
2886	7844	12759		1.12	5.0E-15 UB1328.1	NT	
424	6082	10068		2.43	4.0E-15 AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
							LY1142' Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142' 5' similar to ANF (CARDIOLIPATIN)
4096	9050			7.1	3.0E-15 NR9452.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 SWISSPROT
4770	9754			2.28	3.0E-15 P92485	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
248	5308	10319		2.86	2.0E-15 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
367	5416	10429		2.77	2.0E-15 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
367	5416	10430		2.77	2.0E-16 AF223391.1	NT	h108601.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3142563' similar to contains MER29.b3
2311	7286	12406		1.11	2.0E-15 BE350127.1	EST_HUMAN	MER29 repetitive element; h108601.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3142563' similar to contains MER29.b3
2311	7286	12407		1.11	2.0E-15 BE350127.1	EST_HUMAN	h108601.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3142563' similar to contains MER29.b3
3430	8438	13484		0.91	2.0E-16 AF223391.1	NT	MER29 repetitive element; Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3430	8438	13485		0.91	2.0E-15 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3430	8438	13485		0.91	2.0E-15 AF223391.1	NT	h108601.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741521' 3' similar to contains L1.13 L1
3954	8952	13942		1.02	2.0E-15 AW238499.1	EST_HUMAN	h10708.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2346923' 3' similar to TR-Q61043
4489	9479			2.55	2.0E-15 AI806335.1	EST_HUMAN	Q61043 NINEIN; h228h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745' 3' similar to TR-Q13539 Q13539
2702	7659			1.94	1.0E-15 AI889884.1	EST_HUMAN	MARINER TRANSPOSEASE;
2843	7882			1.78	1.0E-15 BE043684.1	EST_HUMAN	hk40862.y1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2889162' 5'

Page 76 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3069	8085	13089	1.42	1.0E-16 P08547	EST_HUMAN	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4234	9228	14212	0.89	1.0E-16 BE182688.1	EST_HUMAN	RC3-HT0848-100500-022-905 HT0649 Homo sapiens cDNA clone IMAGE:2494590 3'	
4953	9940	14917	0.93	1.0E-15 A1884828.1	EST_HUMAN	WB8604_x1 NCI CGAP_Kid11 Homo sapiens cDNA clone EST384/102 IMAGE sequences, MAGLI Homo sapiens cDNA	
2080	7081		6.06	6.0E-16 AW972811.1	EST_HUMAN	EST384/102 IMAGE sequences, MAGLI Homo sapiens cDNA	
1481	6458	11517	2.3	5.0E-16 AJ251154.1	NT		Mus musculus olfactory receptor cluster, OR37A, OR37C, OR37 genes and OR37D pseudogene
2809	7571	12885	1.58	5.0E-16 AA992178.1	EST_HUMAN	EST384/102 IMAGE sequences, total fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to c80c04_51 Soares total fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to	
2178	7157		0.98	4.0E-16 AB001623.1	NT		contains element L1 repetitive element: Homo sapiens gene for TMEM11 and PWP2, complete and partial cds
2317	7282	12412	1.01	4.0E-16 AW797198.1	EST_HUMAN	CV1-UM0038-200500-115-907 UM0038 Homo sapiens cDNA	
2317	7282	12413	1.01	4.0E-16 AW797198.1	EST_HUMAN	CV1-UM0038-200500-115-912 UM0038 Homo sapiens cDNA	
3375	8383	13403	4.89	4.0E-16 Q166653	SWISSPROT	MYELIN OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR	
4019	9015	14002	4.76	4.0E-16 BE083875.1	EST_HUMAN	PM4-BT0680-010400-002-908 BT0680 Homo sapiens cDNA	
4019	9015	14003	4.76	4.0E-16 BE083875.1	EST_HUMAN	PM4-BT0680-010400-002-909 BT0680 Homo sapiens cDNA	
133	5199	10215	0.97	3.0E-16 AW022862.1	EST_HUMAN	df45c01_y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'	
133	5199	10216	0.97	3.0E-16 AW022862.1	EST_HUMAN	df45c01_y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'	
463	5500		1.75	3.0E-16 AL046445.1	EST_HUMAN	DKFZp434P037_11434 (synonym: hts-3) Homo sapiens cDNA clone DKFZp434P037_11434	
472	6508		2.13	3.0E-16 AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5	
1426	6423	11482	3.78	3.0E-16 Q28983	SWISSPROT	ZONADHESIN PRECURSOR	
2807	7826	12944	4.23	3.0E-16 P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]	
3830	8832	13839	0.78	3.0E-16 T08169.1	EST_HUMAN	EST08080 Infant Brain, Beno Soares Homo sapiens cDNA clone HIBBA13 5' end	
3851	8853		0.67	3.0E-16 AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5	
4785	9769	14753	1.06	3.0E-16 AV861993.1	EST_HUMAN	AV6613B3 GLC Homo sapiens cDNA clone GLCQ3A01 3'	
957	5973		2.44	2.0E-16 AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079	
2817	7579		0.99	2.0E-16 J03061.1	NT	Human SSA1-related endogenous retroviral LTR-like element	
4054	9048	14036	0.92	2.0E-16 X89211.1	NT	Homo sapiens DNA for endogenous retroviral transforming gene protein (PTTG) gene, complete cds	
184	6247	10256	2.54	1.0E-16 AF200719.1	NT	af39g11_51 Soares total fetus Nb2HF8_9w Homo sapiens cDNA clone EST_HUMAN	
381	5456		25.58	1.0E-16 AA628592.1	EST_HUMAN	contains OFR12 OFR repetitive element: Homo sapiens DNA for endogenous retroviral like element	
1927	6913	12009	1.7	1.0E-16 BF321942.1	EST_HUMAN	QV0-BN0148-070705-283-810 BN0148 Homo sapiens cDNA	
3864	8860	13865	3.23	9.0E-17 AW800048.1	EST_HUMAN	CM1-NN1003-200300-153-801 NN1003 Homo sapiens cDNA	
1002	6012		1.93	8.0E-17 AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-801 OT0032 Homo sapiens cDNA	

Page 77 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3787	8800			2.95 1.93	8.0E-17 AL163280.2 7.0E-17 AW983980.1	NT NT	Hom sapiens chromosome 21 segment HS21C080 Mus musculus apolipoprotein B editing complex 2 (Apobec2), mRNA
1431	6428			5.89	8.0E-17 AW983980.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
203	5267	10281		2.71	6.0E-17 T84110.1	EST_HUMAN	ye05h08_r1 Strategene lung #372/10 Homo sapiens cDNA clone IMAGE:1058528 3'
418	5078	10060		0.94	4.0E-17 AA643697.1	EST_HUMAN	mb8605_s1 NCI_CGAP_Cat1 Homo sapiens cDNA clone IMAGE:2604784 3'
3650	6567	13684		1.06	3.0E-17 AW119123.1	EST_HUMAN	xd89c08_x1 Soares_NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
2041	7023	12133		1.31	3.0E-17 P35410	SWISSPROT	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MFG
3121	8137			1.36	3.0E-17 BE328622.1	EST_HUMAN	hw05b04_x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181899 3'
3557	8564	13570		3.0E-17 BE328622.1	EST_HUMAN	hw05b04_x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181899 3'	
3557	8564	13571		1.36	3.0E-17 BE328622.1	EST_HUMAN	qf63a06_x1 NCI CGAP_Ess2 Homo sapiens cDNA clone IMAGE:1956922 3' similar to contains Alt repetitive element
351	5403	10413		2.62	2.0E-17 A1270080.1	EST_HUMAN	qf63a06_x1 NCI CGAP_Ess2 Homo sapiens cDNA clone IMAGE:1956922 3' similar to contains Alt repetitive element
352	5403	10413		2.83	2.0E-17 A1270080.1	EST_HUMAN	qf63a06_x1 Soares_fetal_heart_NbHH18V Homo sapiens cDNA clone IMAGE:398751 3'
973	5999			2.23	2.0E-17 AA722832.1	EST_HUMAN	zg61d04_s1 Soares_fetal_heart_NbHH18V Homo sapiens cDNA clone IMAGE:398751 3'
2379	7361	12471		1.92	2.0E-17 Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2379	7361	12472		1.92	2.0E-17 Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2859	7879			8.43	2.0E-17 P12038	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 kDa NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
3693	8687			4.37	2.0E-17 U52111.2	NT	Hom sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
741	6764	10789		3.03	1.0E-17 P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1670	6666			0.97	1.0E-17 AJ271756.1	NT	Hom sapiens chromosome 21 segment HS21C007
1730	6725	111803		4.26	1.0E-17 AL163207.2	NT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2057	7039	121448		1.51	1.0E-17 P02461	SWISSPROT	Hom sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
2274	7250	12367		2.06	1.0E-17 U78410.1	NT	Hom sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
3488	8496			1.05	1.0E-17 AF224669.1	NT	(UBE2D3) genes, complete cds
4015	9011			8.44	1.0E-17 R09842.1	EST_HUMAN	y30e07_r1 Soares_fetal_liver_spleen cDNA clone IMAGE:128388 6'
3698	8702	13705		8.0E-18	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
347	5399	10407		65.43	7.0E-18 AW316976.1	EST_HUMAN	xx10804_x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb1:20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
347	5399	10408		85.43	7.0E-18 AW316976.1	EST_HUMAN	xx10804_x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb1:20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);

Page 78 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3221 8236	13257	1.08	6.0E-18	X71791.2	NT		Reutis nonneglius partial Gdnf/rn-1 gene for gdnf-derived neuropeptide nebn1, enhancer region
4603 6135		4.28	8.0E-18	P52181	SWISSPROT		PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TG)
1130 5193	11166	11.59	5.0E-18	A1280214.1	EST_HUMAN		grm65g11_x1 Soares_placenta_8daysweeks_2NbHP8t09W Homo sapiens cDNA clone IMAGE:1893668 3'
125 5193	10206	1.37	4.0E-18	BE044076.1	EST_HUMAN		hs36h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3038511 3' similar to contains MER29_b3
125 5193	10207	1.37	4.0E-18	BE044076.1	EST_HUMAN		hs36h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3038511 3' similar to contains MER29_b3
1678 6674	11749	21.73	4.0E-18	AA621844.1	EST_HUMAN		hs36h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3038511 3' similar to contains MER29_b3
2138 7118	12232	0.88	4.0E-18	Q06430	SWISSPROT		hs36h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3038511 3' similar to contains MER29_b3
2138 7118	12233	0.98	4.0E-18	Q06430	SWISSPROT		hs36h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3038511 3' similar to contains MER29_b3
839 5658	10899	34.38	3.0E-18	AA814186.1	EST_HUMAN		hs36h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3038511 3' similar to contains MER29_b3
917 6933	10987	3.2	3.0E-18	BE086834.1	EST_HUMAN		hs36h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3038511 3' similar to contains MER29_b3
3846 8848	13868	1.1	3.0E-18	AL163247.2	NT		hs36h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3038511 3' similar to contains MER29_b3
249 5309	10320	4.3	2.0E-18	AW836820.1	EST_HUMAN		hs36h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3038511 3' similar to contains MER29_b3
1135 6140	21143	2.0E-18	BE258097.1	EST_HUMAN			hs36h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3038511 3' similar to contains MER29_b3
3050 8067	19376	0.93	2.0E-18	Q39575	SWISSPROT		hs36h04_x1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:1205336 6' similar to contains MER29_b3
4291 9283		0.87	1.0E-18	T85406.1	EST_HUMAN		hs36h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER29_b3
541 5576	10582	5.62	9.0E-19	AA281961.1	EST_HUMAN		hs36h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER29_b3
542 5576	10582	3.19	9.0E-19	AA281961.1	EST_HUMAN		hs36h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER29_b3
1031 6041		1.33	8.0E-19	AW974902.1	EST_HUMAN		hs36h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER29_b3
2184 7165	12253	1.86	7.0E-19	4758139	NT		hs36h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER29_b3
3692 8698		1.56	6.0E-19	AW852930.1	EST_HUMAN		hs36h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER29_b3
4339 8330	14314	1.45	6.0E-19	P34986	SWISSPROT		hs36h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER29_b3
4339 9330	14315	1.45	6.0E-19	P34986	SWISSPROT		hs36h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER29_b3

Table 4

Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4635	9840			1.38	8.0E-19 AJ271775.1	NT	Homo sapiens_Xq pseudoblastomeric region; segment 1/2
4895	8845	14820		1.45	6.0E-19 AL120837.1	EST_HUMAN	DKFZp762F182_1/782 (synonym: hmgf2) Homo sapiens cDNA clone DKFZp762F182 5'
550	5584	10586		0.91	4.0E-19 AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2611	7573	12687		1.1	4.0E-19 BF697362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287874 5'
3762	8765	13167		0.98	3.0E-19 Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3762	8765	13168		0.98	3.0E-19 Q28987	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4163	9168	14144		1.07	3.0E-19 O43800	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4163	9168	14145		1.07	3.0E-19 O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4324	8316	14288		1.25	3.0E-19 AV708436.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'
2489	7487	12572		24.97	2.0E-19 AL163201.2	NT	Homo sapiens chromosome 21, segment HS21C001
4323	9315			1.37	2.0E-19 AI311783.1	EST_HUMAN	q691e02_x1 NCI_CGAP_Kle6 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q693886 Q693886
478	5515			1.66	1.0E-19 BE408611.1	EST_HUMAN	q691e02_x1 NCI_CGAP_Kle6 Homo sapiens cDNA clone IMAGE:3638310 5'
2100	7081	12166		1.18	1.0E-19 H30795.1	EST_HUMAN	Human gene for Ah-receptor, exon 7-9
2645	7605			2.01	1.0E-19 D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2774	7795			5.45	1.0E-19 4758977	NT	Human gene for Ah-receptor, exon 7-9
3317	8327	13348		1.46	1.0E-19 AA824987.1	EST_HUMAN	Human gene for Ah-receptor, exon 7-9
3202	8217	13240		0.74	7.0E-20 BF326485.1	EST_HUMAN	PM+AN0086-050800-003-004 AN00866 Homo sapiens cDNA
3478	8486	13505		3.62	6.0E-20 P39188	SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4150	9145	14129		2.85	6.0E-20 BE622434.1	EST_HUMAN	601441231F11 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
4464	9454			1.02	5.0E-20 AV725123.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HTCBTA01 5'
1581	6578	11642		1.44	4.0E-20 AL163247.2	NT	Homo sapiens chromosome 21, segment HS21C047
2078	7060	12170		1.22	3.0E-20 U03888.1	NT	Human BXP21 gene
4088	8082	14073		1.46	3.0E-20 P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 14
4491	9481			1.27	3.0E-20 AA037816.1	EST_HUMAN	zK36612_s1 Scores_Pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to SW:RS5_MOUSE
820	5840			48.46	2.0E-20 AW303868.1	EST_HUMAN	xr24e10_x1 NCI_OGAP_U4 Homo sapiens cDNA clone IMAGE:2781098 3' similar to SW:RS5_MOUSE
1094	6101	11130		3.05	2.0E-20 AA515935.1	EST_HUMAN	P87481_40S_RIBOSOMAL PROTEIN S6_;
1094	6101	11131		3.05	2.0E-20 AA516335.1	EST_HUMAN	ng69n09_s1 NCI_OGAP_Lip2 Homo sapiens cDNA clone IMAGE:940087 similar to TR:G1224068

Page 80 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2745	5840			36.55	2.0E-20 AW303868.1	EST_HUMAN	X24810_x1 NC1 CGAP_U4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW.RS5_MOUSE
4789	9773	14756		4.58	2.0E-20 Q28983	SWISSPROT	P87481 40S RIBOSOMAL PROTEIN S5. ; ZONADHESIN PRECURSOR
4789	9773	14757		4.58	2.0E-20 Q28983	SWISSPROT	ZONADHESIN PRECURSOR
4869	8946			1.73	2.0E-20 5174538 NT	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
1963	7703	12051		2.7	1.0E-20 AA281981.1	EST_HUMAN	Z11d08_r1 NC1 CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.02
4316	8308	14283		1.12	1.0E-20 BF115168.1	EST_HUMAN	211d06_r1 NC1 CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1 repetitive element;
2842	7862			1.16	9.0E-21 AJ003541.4	EST_HUMAN	AJ003541 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MP1pl12-3J21
2016	6999	12102		1.61	7.0E-21 P15600	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMININ) (LAMININ CHAIN B3)
2016	6999	12103		1.61	7.0E-21 P15600	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMININ) (LAMININ CHAIN B3)
4133	9128			6.12	7.0E-21 AA046502.1	EST_HUMAN	2k67a06_r1 Homo sapiens cDNA clone IMAGE:487858 5'
3987	8985	13971		0.88	6.0E-21 BE408611.1	EST_HUMAN	601304125F11 NH_ MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
913	5929	10984		0.78	6.0E-21 59020311 NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4238	8232	14215		3.34	5.0E-21 BE988839.1	EST_HUMAN	6018498771F1 NH_ MGC_74 Homo sapiens cDNA clone IMAGE:39338B0 5'
4548	85229	10984		0.83	5.0E-21 59020311 NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4657	9842	14631		0.35	5.0E-21 4985474 NT	Homo sapiens melanoma antigen, family C-1 (MAGEC1), mRNA	601304125F11 NH_ MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
1698	6691	11787		1.68	4.0E-21 AA970713.1	EST_HUMAN	088608_s1 NC1 CGAP_Kid11 Homo sapiens cDNA clone IMAGE:1157304 3' similar to TR:Q166300 Q16630
1801	6792	11982		1.06	3.0E-21 AL218891.1	EST_HUMAN	PMS3 mRNA ; contains OFR_11 OFR repetitive element ;
2212	7189	12310		0.89	3.0E-21 AL163201.2	NT	Z415d08_s1 Stratagene fetal retina S37202 Homo sapiens cDNA clone IMAGE:628771 3'
3006	8023	13035		3.56	3.0E-21 AL007973.1	NT	Homo sapiens chromosome 21 segment HS21C001
145	5211			18.78	2.0E-21 BE163247.1	EST_HUMAN	QV34T0488-170200-090-912 HT045D Homo sapiens cDNA
922	5828	10969		0.87	2.0E-21 AB007857.2	NT	Hom sapiens mRNA for KIAA0397 protein, partial cds
922	5928	10970		0.87	2.0E-21 AB007857.2	NT	Hom sapiens mRNA for KIAA0397 protein, partial cds
1185	6196			2.36	2.0E-21 BE064410.1	EST_HUMAN	RC4-B10311-1-11189-01-108 BT0311 Homo sapiens cDNA
2567	7530	12848		2.36	2.0E-21 Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2567	7530	12849		2.35	2.0E-21 Q28983	SWISSPROT	ni46cd4_s1 NC1 CGAP_F74 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
1236	6234	11278		1.4	1.0E-21 AA587657.1	EST_HUMAN	MER29 repetitive element;
1378	6376			10.68	1.0E-21 A1601284.1	EST_HUMAN	arr88d12_X1 Barsleed colon HPLRB7 Homo sapiens cDNA clone IMAGE:2260234 3' similar to TR:Q15408 Q15408
4256	9278	14266		1.11	9.0E-22 A1702438.1	EST_HUMAN	CG4a03_s1 NC1 CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2260234 3' similar to NEUTRAL PROTEASE LARGE SUBUNIT ;

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
834	5961		5.16	8.0E-22	BE144748.1	EST_HUMAN	CM0-HT0179-281099-076-h05 HT0179 Homo sapiens cDNA
857	5684	10691	4.8	7.0E-22	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
4160	9165	14138	2.11	7.0E-22	Q611838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
4872	8851	14826	0.98	7.0E-22	AB0108688.1	NT	Homo sapiens gene for activin receptor type IIb, complete cds
3551	8558		13.85	4.0E-22	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region, segment 112
944	6861		0.98	3.0E-22	AJ468679.1	EST_HUMAN	IMAGE:2156611 3' similar to gb:19563 HIGH
2495	7463	12578	2.28	3.0E-22	AI859038.1	EST_HUMAN	IMAGE:2156611 3' similar to gb:19563 HIGH
3588	8595		1.26	3.0E-22	D14718.1	NT	Human chromosomal protein HMG1 related gene
4658	8641	14630	3.17	3.0E-22	AI080125.1	EST_HUMAN	gb:28c07_x1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to
1913	6899		2.09	2.0E-22	NC24942.1	EST_HUMAN	contains MER12.12 MER12 repetitive element;
2452	7422	12537	1.44	2.0E-22	P24816	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
3335	8345	13363	3.9	2.0E-22	8394043	NT	Hom sapiens protein kinase AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
4104	8098	14084	1.53	2.0E-22	AW817784.1	EST_HUMAN	PM1-ST0282-281189-001-012 ST0282 Homo sapiens cDNA
1840	6830	11919	1.41	1.0E-22	AW865517.1	EST_HUMAN	PM4-SN0020-010400-209-h02 SNP020 Homo sapiens cDNA
2507	7475	12580	1.47	1.0E-22	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
3326	8336	13356	1.7	1.0E-22	D14547.1	NT	Human DNA, SINE repetitive element
3238	8251		2.43	7.0E-23	AV847246.1	EST_HUMAN	AV847246 GLC Homo sapiens cDNA clone GLCAV0703'
3349	8358		1.69	6.0E-23	AF198933.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
4146	9141	14125	1.04	6.0E-23	AL163249.2	NT	Human segment HS21C049
5055	8358		1.07	6.0E-23	AF198933.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
658	5685	10692	3.39	2.0E-23	AJ288980.1	NT	Homo sapiens KIAA0851 gene (partial), X3 gene and L2TFL1 gene
1125	7697		3.75	2.0E-23	M55270.1	NT	Human matk/Gia protein (M/GP) gene, complete cds
2723	7680	12793	1.37	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TNX) (HEXBRACHION-LIKE)
2723	7680	12794	1.37	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TNX) (HEXBRACHION-LIKE)
3289	8300		1.07	2.0E-23	AI201458.1	EST_HUMAN	gb:7311.X1 NC_ CGAP_P-28 Homo sapiens cDNA clone IMAGE:1843767 3' similar to TR:Q13537 Q13537
3634	8640		4.12	2.0E-23	BE165980.1	EST_HUMAN	MER3-HT0487-150200-113-901 HT0487 Homo sapiens cDNA
3859	8870	13874	2.39	2.0E-23	H59931.1	EST_HUMAN	Y18602.1 Soares fetal liver spleen INF1S Homo sapiens cDNA clone IMAGE:205418 5'
4397	9388	14371	1.16	1.0E-23	AL163252.2	NT	Y18602.1 Soares fetal liver spleen INF1S Homo sapiens cDNA clone IMAGE:205418 5'
4620	9605		4.78	1.0E-23	AL163210.2	NT	Human segment HS21C010

Page 82 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
548	5582			2.52 1.13	9.0E-24 8.0E-24	AA683213.1 P23269	EST_HUMAN	ab75608.61 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852758 3' similar to TR.E19822 E19822 CA PROTEIN.
4513	9503	14482		4.13	8.0E-24	P23269	SWISSPROT	OLFFACTORY RECEPTOR-LIKE PROTEIN 13
4513	9503	14483		0.83	7.0E-24	AW987884.1	EST_HUMAN	Q00-DT0047-1107200-122-s06 DT0047 Homo sapiens cDNA clone DKFZp434A2311 5'
3781	8784			1.18	7.0E-24	AL039498.1	EST_HUMAN	DKFZp434A2311_11_434 (synonym: hts3) Homo sapiens cDNA clone IMAGE:852758 3' complete cds
4983	9958			2.3	8.0E-24	AB001421.1	NT	Macaaca fasciata mRNA for Testis-Specific Protein Y (TSPY), complete cds
896	5720			32.51	8.0E-24	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
828	5848	10885		8.31	5.0E-24	AJ228043.1	NT	Homo sapiens 559 kb contig between AML1 and CBR1 on chromosome 21q22, segment 313
3863	8885	13889		1.85	3.0E-24	FB08337.1	EST_HUMAN	HSCLRC081 normalized infant brain cDNA Homo sapiens cDNA clone IMAGE:609161 5'
4919	9891	14871		1.8	2.0E-24	AA167589.1	EST_HUMAN	2p11.09.1 Stratagene fetal retina 937202 Homo sapiens cDNA
2285	7261	12379		0.78	2.0E-24	AW898189.1	EST_HUMAN	RC3-NH00884-090560-021-b033 NN0088 Homo sapiens cDNA
3709	8713			2.5	1.0E-24	7706340	NT	Homo sapiens CGI-127 protein (LOC51646), mRNA
1657	6853	11725		1.1	1.0E-24	AWB20194.1	EST_HUMAN	Q00-S70294-00400-185-c7040 S70294 Homo sapiens cDNA
2602	7564			4.21	1.0E-24	D86423.1	NT	Q00-S70294-00400-185-c7040 S70294 Homo sapiens cDNA
2954	7973	12988		1.8	1.0E-24	AF143313.1	NT	Q00-S70294-00400-185-c7040 S70294 Homo sapiens cDNA
4148	9143					ne92e10.s1 NCI CGAP Kid1	1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2	
4837	9821	14798		3.17	7.0E-25	AAA483944.1	EST_HUMAN	MER1 repetitive element;
1612	6808	11672		1.2	5.0E-25	AV850271.1	EST_HUMAN	IL3-C10219-161189-031-D04 CT0219 Homo sapiens cDNA clone IMAGE:1217783 5'
1421	8418	11478		1.64	4.0E-25	T88107.1	EST_HUMAN	Y866h04.1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA
3318	8328			2.89	4.0E-25	AV887671.1	EST_HUMAN	PM3-QT0093-280/200-001-907 OT0093 Homo sapiens cDNA
4180	9183			3.14	4.0E-25	BE170987.1	EST_HUMAN	QV3-HT0543-140400-148-611 HT0543 Homo sapiens cDNA
3246	8269	13280		3.16	3.0E-25	8923321	NT	(Homo sapiens hypothetical protein FLJ20344), mRNA
3246	8259	13281		3.16	3.0E-25	8923321	NT	(Homo sapiens hypothetical protein FLJ20344), mRNA
1329	6327	11375		3.49	2.0E-25	5032158	NT	(Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2245	7222	12341		8.05	2.0E-25	BE888016.1	EST_HUMAN	601511630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
2758	7440						40S RIBOSOMAL PROTEIN S16	
4068	9060	14047					40S RIBOSOMAL PROTEIN S16	
4068	9060	14048					40S RIBOSOMAL PROTEIN S16	
363	6412	10125					40S RIBOSOMAL PROTEIN S16	
1229	6226						40S RIBOSOMAL PROTEIN S16	
2367	7341	12458					40S RIBOSOMAL PROTEIN S16	
4710	9695	14678					40S RIBOSOMAL PROTEIN S16	
2412	7383	12502					40S RIBOSOMAL PROTEIN S16	

Page 83 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							Regions	Regions
1542	6540	11597	1.66	7.0E-26	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	
3873	8874	13876	1.32	7.0E-26	X89211.1	NT	H sapiens DNA for endogenous retroviral like element	
4035	9031	14018	1.76	7.0E-26	AW240153.1	EST_HUMAN	hsd2e12.x1 Scares	cDNA clone IMAGE:28083766 3'
2164	7143	12261	9.02	6.0E-26	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families	
3271	8283	13306	1.78	6.0E-26	AA20613.1	EST_HUMAN	Zp72h04.r1 Stereogene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:345271 5'	
1158	6162	11198	6.17	5.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to	
1158	6162	11197	5.17	5.0E-26	AI708235.1	EST_HUMAN	WP:F49C12.11 CEO03371;	
1721	8716	11792	1.25	3.0E-26	D14547.1	NT	Human DNA, SINE repetitive element	
1881	6965		2.26	3.0E-26	AA115895.1	EST_HUMAN	2n30d08.r1 Stereogene neuroepithelium NT2RAMI 837234 Homo sapiens cDNA clone IMAGE:548943 5'	
3691	8695	18697	1.2	3.0E-26	AA152464.1	EST_HUMAN	G685374 THYROID RECEPTOR PRECURSOR (HUMAN);	
3691	8695	13698	1.2	3.0E-26	AA152464.1	EST_HUMAN	zg30f10.r1 Stereogene colon (#837204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G685374	
673	6698	10707	5.99	2.0E-26	AL163282.2	NT	G685374 THYROID RECEPTOR INTERACTOR;	
1831	6621		2.34	2.0E-26	AL035099.2	EST_HUMAN	DKFZp566L171_s1_566 (synonym: hk5d2) Homo sapiens cDNA clone DKFZp566L171 3'	
3160	8176	13199	5.27	2.0E-26	X86604.1	NT	M.musculus mRNA for astrotcytic phosphoprotein, PEA-15	
137	6203	10218	68.33	1.0E-26	BE170371.1	EST_HUMAN	QV4-HT0538-020300-123-a02 H10538 Homo sapiens cDNA	
2492	7460	12575	1.04	1.0E-26	BE149855.1	EST_HUMAN	MF2-BN0114-240500-030-307 BN0114 Homo sapiens cDNA	
2816	7677		57.21	1.0E-26	AF261985.1	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds	
11	6091	10076	2.7	8.0E-27	AI831462.1	EST_HUMAN	Wf48c04.x1 NCI CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408160 3' similar to 6b:K00558	
553	5587		2.73	8.0E-27	AI163227.2	NT	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783285 3' similar to 6b:K00558	
1391	6388	11440	83.09	8.0E-27	AW162237.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN);	
1391	6388	11441	83.09	8.0E-27	AW162237.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783285 3' similar to 6b:K00558	
2103	7083	12188	1.71	8.0E-27	AW864776.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN);	
3111	8127	13147	2.68	8.0E-27	P12236	SWISSPROT	PM2-SN0018-220300-002-a07 SN0018 Homo sapiens cDNA	

Page 84 of 209

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (T _{Cap}) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
675	6700		1.35	7.0E-27	Z70864.1	NT	Human endogenous retroviral element HC22
4918	9898		2.5	7.0E-27	AW629172.1	EST_HUMAN	NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975878 3' similar to TR:O76040
1990	6975	12050	2.62	3.0E-27	X60638.1	NT	h51h12.x1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975878 3' similar to TR:O76040 ORF2; FUNCTION UNKNOWN; Rattus RY43 mRNA for a potential ligand-binding protein
4149	8144	14128	1.28	3.0E-27	BE071924.1	EST_HUMAN	FMD:BT0527-090100-001-011 B10527 Homo sapiens cDNA
42	51222	10110	36.88	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1855	6844		37.38	2.0E-27	AA585345.1	EST_HUMAN	h501b1.51 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:NM178888 60S rRNA
3036	8053		10.83	2.0E-27	AW629172.1	EST_HUMAN	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
3153	8169	12189	1.89	2.0E-27	AF111167.2	NT	h51h12.x1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975878 3' similar to TR:O76040
3153	8169	13180	1.99	2.0E-27	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; c-fos gene, complete cds; and unknown gene
433	6471		1.55	1.0E-27	AL163246.2	NT	h51h12.x1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975878 3' similar to TR:O76040
881	5996	11028	1.2	1.0E-27	AB026898.1	NT	Homo sapiens chromosome 21 segment HS21C046
3966	8984		1.02	1.0E-27	BE260127.1	EST_HUMAN	h51h12.x1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975878 3' similar to TR:O76040
141	5206		2.16	9.0E-28	BE348389.1	EST_HUMAN	SECRETED NEUREXIN III_ALPHAC PRECURSOR; [3] TR:Q07313 ;
309	5364	10375	2.37	9.0E-28	AU126280.1	EST_HUMAN	AL126280 NT2RP1 Homo sapiens cDNA clone NT2RP1000443 5'
1162	6166	11200	15.2	7.0E-28	AU112750.1	EST_HUMAN	AL142750 Y78AA1 Homo sapiens cDNA clone Y78AA1000824 5'
316	5371		2.32	5.0E-28	A192103.1	EST_HUMAN	Y168R10.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR:51
3902	8902	13900	1.88	5.0E-28	R79162.1	EST_HUMAN	Y168R10.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR:51
2552	7517	128335	2.12	4.0E-28	AW186066.1	EST_HUMAN	Y168R10.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR:51
2808	7827	128445	1.09	4.0E-28	46505316	NT	Y168R10.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR:51
3035	8052	13061	5.85	4.0E-28	BE409100.1	EST_HUMAN	Y168R10.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR:51
1284	6282		1.88	3.0E-28	AF155382.1	NT	Y168R10.r1 Scores placenta Nb2HP Homo sapiens cDNA
87	5184	10175	8.92	2.0E-28	BE062187.1	EST_HUMAN	RC1-BT0264-220300-019-c05 BT0254 Homo sapiens cDNA
1147	6151	11183	10.35	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41

Page 85 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe	Exon	ORF seq	Most Similar	Top Hit	Top Hit	Top Hit
SEQ ID	SEQ ID	ID NO:	(Top) Hit BLAST E	Accession No.	Database Source	Descriptor
NO:	NO:		Value			
						q05508.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1810483 3' similar to contains 11_b2_L1
2405	7376	12468	1.68	2.0E-28	AI348634.1	EST_HUMAN
3281	8293	13318	0.68	2.0E-28	AL163209.2	NT
1448	6445	11604	1.71	1.0E-28	D38044.1	EST_HUMAN
2158	7137	12268	2.04	1.0E-28	BF332361.1	EST_HUMAN
4436	9426		2.22	1.0E-28	U09410.1	NT
5003	9874	14949	1.55	1.0E-28	P23275	SWISSPROT
1567	6584	11627	1.17	7.0E-29	AW966447.1	EST_HUMAN
3476	8484		1.34	7.0E-29	BE254703.1	EST_HUMAN
590	5821	10620	9.68	8.0E-29	AI936748.1	EST_HUMAN
4839	9823		1.37	6.0E-29	AL163203.2	NT
3161	8177		1.75	4.0E-29	AI752367.1	EST_HUMAN
4280	9282	14270	1.29	3.0E-29	AB042297.1	NT
489	5525	10632	1.16	2.0E-29	AF084899.1	NT
		10533	1.15	2.0E-29	AF084899.1	NT
1501	8499	11653	4.66	2.0E-29	AI963604.1	EST_HUMAN
1501	8499	11554	4.66	2.0E-29	AI963604.1	EST_HUMAN
4157	9152	14134	2.09	2.0E-29	AI163288.2	NT
1484	6481		1.34	7.0E-30	BE091133.1	EST_HUMAN
1534	6532		0.9	6.0E-30	X51755.1	NT
1736	6731	11808	1.1	8.0E-30	D25303.1	EST_HUMAN
3117	8133	13162	2.42	6.0E-30	BE008028.1	EST_HUMAN
4614	8133	13162	0.93	6.0E-30	BE008028.1	EST_HUMAN
3906	8806		40.12	5.0E-30	A1389892.1	EST_HUMAN
2082	7063	12172	1.93	4.0E-30	AW897471.1	EST_HUMAN
2082	7063	12173	1.93	4.0E-30	AW897471.1	EST_HUMAN
1134	8139		3.35	3.0E-30	AI339551.1	EST_HUMAN
3672	8677	13680	0.82	3.0E-30	AF128893.1	NT

PCT/US01/00661

Page 86 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
687	5692	10701	1.21	2.0E-30	AW857315.1	EST_HUMAN	CM0-C70307-310100-158-h03 CT0307 Homo sapiens cDNA
1088	6076		2.46	2.0E-30	F08888.1	EST_HUMAN	HSC28F051 normalized infant brain cDNA Homo sapiens cDNA clone c-2305
1449	6448	11505	8.55	2.0E-30	BE175877.1	EST_HUMAN	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2643	7803	12716	6.5	2.0E-30	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
2849	7869	12885	6.88	2.0E-30	AF114156.1	NT	Homo sapiens Y-linked zinc finger protein (ZF-1) gene, complete cds
3700	8704	13707	2.23	2.0E-30	AW206581.1	EST_HUMAN	U1-H-B11-efc-6-12-0-U1-s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4833	9818	14609	1.61	2.0E-30	BE288945.1	EST_HUMAN	6011198860f1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
4633	9818	14610	1.61	2.0E-30	BE288945.1	EST_HUMAN	6011198860f1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
284	5342	10355	13.84	1.0E-30	C16839.1	EST_HUMAN	C16839 Human placenta cDNA (TF-1) Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains
533	5568	10871	3.42	1.0E-30	AW488897.1	EST_HUMAN	hd0504_x1_Scores_NFL_T_GEC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains
708	5730	10746	3.16	1.0E-30	AL169203.2	NT	ME113 MER1 repetitive_element:
2150	729	12248	2.78	1.0E-30	AA684377.1	EST_HUMAN	hs77608_s1 Stratagene lung (#S37210) Homo sapiens cDNA clone IMAGE:3685698 3'
2383	7384	12488	1.95	1.0E-30	BF347728.1	EST_HUMAN	602022860f1 NCI_CGAP_Bm37 Homo sapiens cDNA clone IMAGE:4157891 5'
2980	7898	13011	0.78	1.0E-30	AA315045.1	EST_HUMAN	EST186868 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end
1060	8089	11100	8.71	8.0E-31	89233899	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2347	7321		23.47	8.0E-31	AL168208.2	NT	Homo sapiens chromosome 21 segment HS21C008
4763	8147	14733	1.01	8.0E-31	P23275	SWISSPROT	OLFACTOORY RECEPTOR_16 (OR3)
4763	8147	14734	1.01	8.0E-31	P23275	SWISSPROT	OLFACTOORY RECEPTOR_16 (OR3)
701	5125		2.43	7.0E-31	AA372687.1	EST_HUMAN	ESTB4555 Colorectal adenocarcinoma IV Homo sapiens cDNA 5' end
2597	7559	12676	2.16	7.0E-31	BE5226517.1	EST_HUMAN	hs05611-x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
3594	8601		2.5	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-9, and partial cds, alternatively spliced
192	5256	10288	3.17	5.0E-31	MG0694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
192	5256	10289	3.17	5.0E-31	MG0694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
691	5622		3.18	4.0E-31	AJ271735.1	NT	Homo sapiens Xg pseudautosomal region, segment 1/2
1782	6774		1.4	4.0E-31	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2716	7673		1.63	4.0E-31	6730038	NT	Homo sapiens SET domain endonuclease component (SETMAR) mRNA
2519	7488	12804	1.54	3.0E-31	6005871	NT	Homo sapiens SEC63, endoplasmic reticulum translocon component (S. cerevisiae) like (SEC63L), mRNA
1873	6862	11951	2.35	2.0E-31	AW838171.1	EST_HUMAN	Q72-L70051-26030-111403 L70051 Homo sapiens cDNA
2162	7131	12248	1.01	2.0E-31	A1388988.1	EST_HUMAN	1944905-x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3'
2278	7254	12373	1.62	2.0E-31	AL119245.1	EST_HUMAN	DIK72p701G1513_r1 781 (synonym: hamy2) Homo sapiens cDNA clone DKF7p701G1513 5'

Page 87 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2373	7345	12485	4.03	2.0E-31	AA458824.1	EST_HUMAN	aa88f11_s1 Strategens fetal retina S37202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR_12 THR repetitive element; Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
16	5085	10079	10.14	1.0E-31	U93163.1	NT	
1623	6820	11686	9.06	1.0E-31	095371	SWISSPROT	OLFFACTORY RECEPTOR 2C1
1623	6820	11687	9.05	1.0E-31	095371	SWISSPROT	OLFFACTORY RECEPTOR 2C1
1623	6820	11688	8.05	1.0E-31	095371	SWISSPROT	OLFFACTORY RECEPTOR 2C1
1623	6820	14467	1.26	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_11_547 (synonym: hb11) Homo sapiens cDNA clone DKFZp547B235_5'
4501	9491	14468	1.26	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_11_547 (synonym: hb11) Homo sapiens cDNA clone DKFZp547B235_5'
4501	9491	14469	1.26	1.0E-31	AL134376.1	EST_HUMAN	ctz15a9_xl Scores_fetal liver spleen_1NFL_S_1 Homo sapiens cDNA clone IMAGE:1675384 3'
2024	7007	12113	5.49	8.0E-32	AI056770.1	EST_HUMAN	Homo sapiens PRO1181 mRNA, complete cds
1017	6027	11057	84.59	5.0E-32	AF116827.1	NT	Homo sapiens chromosome 21 segment HS21C046
918	5924		1.7	4.0E-32	AL163246.2	NT	Homo sapiens FLL-1 gene, partial
453	5480	10505	2.46	3.0E-32	Y17298.1	NT	Homo sapiens cDNA clone HTFAK007 5'
1427	6424	11483	57.22	3.0E-32	AV731500_HTF	EST_HUMAN	AV731500_HTF Homo sapiens complete cds
2604	7586		1.49	1.0E-32	DB4430.1	NT	Homo sapiens mRNA for phenylalanyl tRNA synthetase, complete cds
3020	8037		1.65	1.0E-32	BE743299.1	EST_HUMAN	BE743299.1 Homo sapiens cDNA clone IMAGE:3834433 5'
3400	8409		5.22	9.0E-33	BE327112.1	EST_HUMAN	HW0705_x1_NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:3162216 3' similar to TR:Q88539 Q88539
62	5142	10144	11.74	7.0E-33	5031736_NT	NT	WW DOMAIN BINDING PROTEIN 11.1
62	5142	10145	11.74	7.0E-33	5031736_NT	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2097	7078	12192	1.93	7.0E-33	AI590115.1	EST_HUMAN	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2576	7539		7.4	7.0E-33	AV730056.1	EST_HUMAN	AV730056_HTF Homo sapiens cDNA clone HTFANF08 5'
2751	6655	11727	1.01	7.0E-33	AV730015.1	EST_HUMAN	EST7383396 MAGE sequences, MAGL Homo sapiens mRNA
3168	8184		14.85	7.0E-33	AW971307.1	EST_HUMAN	EST7383396 MAGE sequences, MAGL Homo sapiens mRNA
3652	8858		0.8	6.0E-33	AL163245.2	NT	HS21C085
1740	6735		1.43	5.0E-33	BT375315.1	EST_HUMAN	QV1-F10169-100700-271-a02 FT0159 Homo sapiens cDNA
1842	6832		0.97	5.0E-33	11141884	NT	member 7 (SLC6A7), mRNA
1858	6847	11824	4.15	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1858	6847	11825	4.15	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
2210	7187		1.61	5.0E-33	AL163285.2	NT	Hom sapiens chromosome 21 segment HS21C085
3945	8943	13933	1.87	5.0E-33	AB014689.1	NT	Hom sapiens mRNA for KIAA0689 protein, partial cds
5065	10034	16001	1.07	5.0E-33	M64350.1	NT	Human TCR variable region Vα30 subfamily gene (VΑ30), JA, CA segments, 5' end
1111	6117		1.87	4.0E-33	AL163207.2	NT	Hom sapiens chromosome 21 segment HS21C007

Page 88 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2066	7048	12166	1.87	4.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2353	7327		1.14	4.0E-33	AA628621.1	EST_HUMAN	ab51b11_r1 Strategene lung carcinoma 93718 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28 repetitive element;
2474	7443	12658	2.2	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4356	9347	14927	1.46	4.0E-33	AW283349.1	EST_HUMAN	U1-H-B12-ah1-c-03-U1.s1 NCI_LGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
1073	6081		5.08	3.0E-33	BE350127.1	EST_HUMAN	h08601_x1 NCI_LGAP_Kid13 Homo sapiens cDNA clone IMAGE:3143256 3' similar to contains MER28.b3
1074	6081		3.92	3.0E-33	BE350127.1	EST_HUMAN	h08601_x1 NCI_LGAP_Kid13 Homo sapiens cDNA clone IMAGE:3143266 3' similar to contains MER28.b3
2382	7770		1.73	3.0E-33	AV647851.1	EST_HUMAN	MER28 repetitive element; AV647851 GLC Homo sapiens cDNA clone GLCBCF09 3'
16	5098		1.02	2.0E-33	AI160189.1	EST_HUMAN	qb67g03_x1 SacCes fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR11 OFR repetitive element;
105	5098		2.37	2.0E-33	AI160189.1	EST_HUMAN	qb67g03_x1 SacCes fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR11 OFR repetitive element;
4295	9287		6.1	2.0E-33	BE156029.1	EST_HUMAN	MRO-H10405-160300-202-008 H10405 Homo sapiens cDNA clone IMAGE:844388 5' similar to ab51g11_r1 Strategene lung carcinoma 83718 Homo sapiens cDNA clone IMAGE:844388 5' similar to
4826	9810	14791	30.71	2.0E-33	AA628683.1	EST_HUMAN	gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
4922	9800	14876	2.2	2.0E-33		NT	Homo sapiens hypothetical protein SIRP-52 (SIRP-b2), mRNA
4922	9800	14876	2.2	2.0E-33		NT	Homo sapiens hypothetical protein SIRP-52 (SIRP-b2), mRNA
9	5089		1.61	1.0E-33	AF003628.1	NT	Homo sapiens X-linked arthrogryposis ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4368	9360	14340	1.09	8.0E-34	BE062570.1	EST_HUMAN	QV2-B70258-071289-016-g107 BT0258 Homo sapiens cDNA
1419	6416	11476	2.31	7.0E-34	T70845.1	EST_HUMAN	jd15c05_r1 SacCes fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
468	5504	10517	1.48	6.0E-34	U10981.1	NT	Human G2 protein mRNA, partial cds
468	6504	10518	1.48	6.0E-34	U10981.1	NT	Human G2 protein mRNA, partial cds
1841	6831		2.53	5.0E-34	77056500	NT	Homo sapiens NpwpB-binding protein NpwpB (LOC51729), mRNA
4893	9872	14839	5.04	5.0E-34	U30983.1	NT	Human splicing factor SRp55-1 (SRp-55) mRNA, complete cds
1982	6838	12040	1.36	4.0E-34	AI804687.1	EST_HUMAN	h84c06_x1 NCI_LGAP_P728 Homo sapiens cDNA clone IMAGE:2249194 3'
2847	7807	12719	0.92	4.0E-34	8922807	NT	Homo sapiens hypothetical protein FLJ10888 (FLJ10888), mRNA
3089	8115	13133	1.38	4.0E-34	5803166	NT	Homo sapiens splicing factor 3a, subunit 3, 80kD (SF3A3), mRNA
1475	6472	11530	14.56	1.0E-34	P12236	SWISSPROT	ADP ATP CARRIER PROTEIN LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3569	8596	13600	1.32	1.0E-34	AF003528.1	NT	Homo sapiens X-linked arthrogryposis ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3957	8955	13944	0.83	1.0E-34	AY008397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
3957	8955	13945	0.93	1.0E-34	AY008397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4352	9343		4.5	1.0E-34	BE071414.1	EST_HUMAN	RC2-B/T056-240400-016-h08 B/T056 Homo sapiens cDNA
3560	8567	13573	1.41	9.0E-35	AW663302.1	EST_HUMAN	hh77b06.y1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868787 6'
224	5286		25.01	8.0E-35	6031190	NT	Homo sapiens prohibitin (PHB) mRNA
1659	6694	11770	2.3	8.0E-35	BF569837.1	EST_HUMAN	naa33a03.x1 NCI CGAP_Kid1 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:075912
1659	6694	11771	2.3	8.0E-35	BF569837.1	EST_HUMAN	naa33a08.x1 NCI CGAP_Kid1 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:075912
4717	9702	14888	3.04	8.0E-35	BF183195.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE (OTA);
1388	6385	11437	1.5	6.0E-35	AA757115.1	EST_HUMAN	at53103.s1 Searles testis NHT Homo sapiens cDNA clones 1309397 3'
1825	6911	12006	1.65	6.0E-35	60059975	NT	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
6083	10032		0.75	6.0E-35	8823389	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
1671	6667	11742	1.53	5.0E-35	X63392.1	NT	H.sapiens Immunoglobulin kappa light chain variable region L14
2711	7668	12781	1.05	5.0E-35	AB007868.2	NT	Homo sapiens mRNA for KIAA0786 protein, partial cds
2839	7859	12977	1.22	5.0E-35	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
4285	9277	14285	1.3	5.0E-35	AF023268.1	NT	Homo sapiens cik2 kinase (CLK2), prop1, cote1, glucocerebrosidase (GBA), and metaxin genes, complete cds; metaxin pseudogene and glucocerebrosidase pseudogene; and thrombospondin (THBS3) gene, partial cds
1408	6406	11463	66.29	4.0E-35	BE257807.1	EST_HUMAN	601109719F1 NIH MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
1783	6775	11866	19.99	4.0E-35	HB1193.1	EST_HUMAN	yu93a07.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:241238 5' similar to contains PTR5 repetitive element;
1544	6542	11600	52.74	3.0E-35	BE268182.1	EST_HUMAN	601125260F11 NIH MGC_8 Homo sapiens cDNA clone IMAGE:3345663 5'
2289	7246		1.68	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
108	7713	10192	1.21	2.0E-35	N88985.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPLICATIVE ELEMENT
1168	6171	11203	1.09	2.0E-35	T11909.1	EST_HUMAN	A971F Heart Homo sapiens cDNA clone A971
2156	7135	12254	2.74	2.0E-35	AB018413.1	NT	Homo sapiens mRNA for Gab2, complete cds
2812	7574	12688	1.82	2.0E-35	AW663005.1	EST_HUMAN	h186a12.x1 Soares_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:28791683 similar to SW TR12_HUMAN Q14669 THYROID RECEPTOR INTERACTING PROTEIN 12;
3480	8488		0.84	2.0E-35	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
3814	8817	13823	0.81	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP452B

Page 90 of 209

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3814	8817	13824	0.81	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E3328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBAA Homo sapiens cDNA clone TCBAP4328
4535	9525		2.63	2.0E-35	H49239.1	EST_HUMAN	Yq19a12_r1 Soares fetal liver spleen INF1S Homo sapiens cDNA clone IMAGE:274079 5'
47	5128	10119	6.23	1.0E-35	AA681949.1	EST_HUMAN	fmic16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
47	5129	10120	6.23	1.0E-35	AA681949.1	EST_HUMAN	fmic16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
743	5786	10780	140.65	1.0E-35	AW386473.1	EST_HUMAN	IL2-ST0162-131099-008-d12 ST0162 Homo sapiens cDNA SP:AA44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
743	5765	10791	140.65	1.0E-35	AW386473.1	EST_HUMAN	IL2-ST0162-131099-008-d12 ST0162 Homo sapiens cDNA SP:AA44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
898	5916		1.2	1.0E-35	T87947.1	EST_HUMAN	Yd38a01_r1 Soares fetal liver spleen INF1S Homo sapiens cDNA clone IMAGE:115752 5' similar to
2471	7439	12655	2.17	1.0E-35	7705894	NT	Homo sapiens hypothetical protein (LOC5233), mRNA
2694	7652	12766	1.37	1.0E-35	BE350127.1	EST_HUMAN	h109g01_x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29_d3
2694	7652	12787	1.37	1.0E-35	BE350127.1	EST_HUMAN	h109g01_x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29_d3
3070	8089	13100	1.24	1.0E-35	6006030	NT	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L) mRNA
3080	8106	13121	2.49	1.0E-35	AV650422	GLC_Homo sapiens cDNA clone GLCCEFF08 3'	AV650422 GLC_Homo sapiens cDNA clone GLCCEFF08 3'
3080	8108	13122	2.49	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC_Homo sapiens cDNA clone GLCCEFF08 3'
4288	9280	14216	4.67	1.0E-35	7656805	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
4288	9280	14277	4.67	1.0E-35	7656805	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
3879	8880	13883	1.76	8.0E-36	AW821707.1	EST_HUMAN	RC3-ST0315_1802200-013-f12 ST0315 Homo sapiens cDNA
2860	7850	12898	2.3	7.0E-36	AW857579.1	EST_HUMAN	CM1-C10315_091289-053-d07 CT0315 Homo sapiens cDNA
3044	8061		4.78	7.0E-36	4557498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
1957	6943	12045	1.89	8.0E-36	77058622	NT	Homo sapiens nitroarginin 2 (NINJ2), mRNA
2351	7325		5.02	8.0E-36	AB035348.1	NT	Homo sapiens TCF16 gene, exon 12
3554	8561	13667	1.16	6.0E-36	BF515101.1	EST_HUMAN	Ui-H-BW1-anv-c-12-0-Ui_1 r NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
138	5224	10219	10.77	6.0E-36	A1277135.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2678	7656	12751	24.78	5.0E-36	BE388436.1	EST_HUMAN	6012855677F_NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3807289 5'
3531	8537	13642	1.37	5.0E-36	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4643	9628	14621	2.22	5.0E-36	6728728	NT	Homo sapiens API5-like 1 (AP15L1), mRNA
4643	9628	14622	2.22	5.0E-36	5728729	NT	Homo sapiens API5-like 1 (AP15L1), mRNA
1205	6206	11243	2.05	4.0E-36	BE010038.1	EST_HUMAN	IPM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1416	8413	11474	1.38	4.0E-36	P10266	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1606	6802	11664	1.78	4.0E-36	BE382374.1	EST_HUMAN	601285574F_NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3828386 5'

Page 91 of 209
Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
2161	7140		4.99	4.0E-36	AW247712.1	EST_HUMAN	282020_Spintris NIH_MGC_7 Homo sapiens cDNA clone IMAGE:28202020 5'	
3276	8287	13311	0.98	4.0E-36	BE389299.1	EST_HUMAN	601282286F NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3804468 5'	
3275	8287	13312	0.98	4.0E-36	BE389298.1	EST_HUMAN	601282256F NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3804468 5'	
687	5711	10725	2.91	3.0E-36	AF088810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds	
1468	6465	11624	1.3	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds	
1468	6465	11625	1.3	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds	
2235	7212	12329	2.14	3.0E-36	7882401	NT	Homo sapiens KIAA0932 protein (KIAA0932), mRNA	
4373	8865	14346	6.39	3.0E-36	10181139	NT	Homo sapiens Luracothophilin 1 (Jpi-Pending), mRNA	
3098	8112	13130	6.85	2.0E-36	BE269287.1	EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342708 5'	
4802	9788	14788	17.88	2.0E-36	AW880376.1	EST_HUMAN	QV6-OT0030-240300-174-H04 OT0030 Homo sapiens cDNA	
874	56892	109833	1.87	1.0E-36	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:36335480 5'	
2084	7065	12176	1.85	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131189-021-h07 HT0217 Homo sapiens cDNA	
2084	7065	12177	1.85	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131189-021-h07 HT0217 Homo sapiens cDNA	
2139	7119	12234	1.5	1.0E-36	BF675781.1	EST_HUMAN	602136493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5'	
3269	8282			1.42	1.0E-36	AF156982.1	NT	Homo sapiens human endogenous retrovirus W proC8-19 protease (pro) gene, partial cds
3276	8288	13313	0.98	8.0E-37	4757879	NT	Homo sapiens chitinase (chitinase) 2 (CHI2) mRNA	
1265	6283	2.88	7.0E-37	AL042800.1	EST_HUMAN	DKFZp434E0422_r1434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0422 5'		
1705	6700	11776	1.1	7.0E-37	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; ctfos gene, complete cds; and unknown gene	
1705	6700	11777	1.1	7.0E-37	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; ctfos gene, complete cds; and unknown gene	
4955	5932		1.57	6.0E-37	RI103391	EST_HUMAN	Y125a02.11 Scares fetal liver spleen INF3 Homo sapiens cDNA clone IMAGE:127850 5'	
2357	7331	12447	2.14	4.0E-37	AA702784.1	EST_HUMAN	Z190b04.51 Soares_fetal_liver_spleen_1NFS_S1 Homo sapiens cDNA clone IMAGE:448015 3'	
5038	10009		0.91	4.0E-37	N82051.1	EST_HUMAN	ESTS2910 WATM1 Homo sapiens cDNA clone B2g10 similar to human STS G04101	
1987	6952	12056	1.95	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418	
1987	6952	12057	1.95	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418	
2441	7411		1.2	3.0E-37	AW6861150.1	EST_HUMAN	EST373222 MAGE resequences, MAGF Homo sapiens cDNA	
2895	7814		3.82	3.0E-37	AW6861150.1	EST_HUMAN	EST1373222 MAGE resequences, MAGF Homo sapiens cDNA	
4831	8815		0.76	3.0E-37	BF035327.1	EST_HUMAN	601456531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3882086 5'	
380	6455	10472	1.71	2.0E-37	D89780.1	NT	Homo sapiens mRNA for AMI_1, complete cds	
380	6455	10473	1.71	2.0E-37	D89780.1	NT	Homo sapiens mRNA for AMI_1, complete cds	
1084	6072	11104	2.16	2.0E-37	AU131202.1	EST_HUMAN	AUJ31202 NT2RP3 Homo sapiens cDNA clone NT2RP3002168 5'	

Table 4

Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1084	6072	11105	2.16	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RPG Homo sapiens cDNA clone N12RPG3002166 5'
1923	6909	12004	1.46	2.0E-37	AL163247.2	NT	Hom sapiens chromosome 21 segment HS21C047
3798	8801	13808	4.94	2.0E-37			Hom sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebromitinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
4123	9118	14104	0.78	2.0E-37	4826685	NT	Hom sapiens DEAD1H (Asp-Glu-Ala-Asp1His) box polypeptide 1 (DDX1) mRNA
2034	7017	12127	3.69	1.0E-37	AL163281.2	NT	Hom sapiens chromosome 21 segment HS21C081
3124	8140		0.98	1.0E-37	AW862082.1	EST_HUMAN	RC3-CT0347-210400-016-h03 CT0347 Homo sapiens cDNA
3885	8857	13863	1.18	1.0E-37	AF189011.1	NT	Hom sapiens ribonuclease III (RN3) mRNA, complete cds
4783	9767	14751	2.02	1.0E-37	BF371719.1	EST_HUMAN	QVO-FN0180-280700-318c-10 FN0180 Homo sapiens cDNA
1202	6203	11240	1.69	8.0E-38	11436955	NT	Hom sapiens Grib2-associated blinder 2 (KIAA0571) mRNA
2425	7396	12517	1.23	8.0E-38	BF346221.1	EST_HUMAN	802018401F1 NCI CGAP Bm67 Homo sapiens cDNA clone IMAGE4153982 5'
2119	7089	12212	6.28	7.0E-38	AW972825.1	EST_HUMAN	EST384920 MAGE resequences, MAGL Homo sapiens cDNA
2869	7887	13001	2.89	6.0E-38	BF033033.1	EST_HUMAN	601455722F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE3866348 5'
717	5740	10757	1.86	5.0E-38	AW871819.1	EST_HUMAN	EST383808 MAGE resequences, MAGL Homo sapiens cDNA
2385	7356	12476	4.11	5.0E-38	AJ237740.1	NT	Hom sapiens RIBIR gene (partial), exon 8
4891	7356	12478	1.09	5.0E-38	AJ237740.1	NT	Hom sapiens RIBIR gene (partial), exon 8
119	5189	10200	3.97	4.0E-38	Z25468.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
119	5189	10201	3.97	4.0E-38	Z25468.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
2043	7025		2.4	3.0E-38	AF003530.1	NT	Hom sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3613	8620		1.58	3.0E-38	7649807	NT	Hom sapiens HIRA interacting protein 4 (dmd1-like) (HIRIP4), mRNA
3765	8768	13772	1.58	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3765	8769	13773	1.58	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
4482	9472		1.26	3.0E-38	BE279301.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE3504272 5'
51	5132	10127	1.71	2.0E-38	AL163248.2	NT	Hom sapiens chromosome 21 segment HS21C048
1361	6358	11403	8.04	2.0E-38			Hom sapiens SMT3 (suppressor of mif No 3, yeast) homolog 2 (SMT3H2), mRNA
1607	6603	11685	1.7	2.0E-38	AA437353.1	EST_HUMAN	SWMA12_RABBIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1-2-MANNOSIDASE ;
1607	6603	11686	1.7	2.0E-38	AA437353.1	EST_HUMAN	SWMA12_RABBIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1-2-MANNOSIDASE ;
3465	8463		0.81	2.0E-38	AF070970.1	NT	Hom sapiens protein phosphatase 2C alpha 2 mRNA, complete cds
4448	8438	14421	6	2.0E-38	4657887	NT	Hom sapiens keratin 18 (KRT18) mRNA
4953	9830	14809	0.76	2.0E-38	BE286224.1	EST_HUMAN	601177386F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE3532560 5'
4853	9830	14910	0.75	2.0E-38	BE286224.1	EST_HUMAN	601177386F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE3532560 5'

Page 93 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1076	6083		1.97	1.0E-38	AA401570.1	EST_HUMAN	zj6202_r1_Scares_testicular cDNA clone IMAGE:742539 5' similar to contains element MER18 repetitive element;
1953	6939	12041	3.28	1.0E-38	4885288	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
1970	6955	12059	0.96	1.0E-38	7661969	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
2423	7394	12515	2.9	1.0E-38	AF270831.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
4192	9185	14166	0.72	1.0E-38	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 8 (LRP8) mRNA, and translated products
4197	9190	14171	1.27	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4197	9190	14172	1.27	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4466	9456	14436	1.06	1.0E-38	8922563	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
55	6136	10133	6.42	8.0E-39	4502312	NT	Homo sapiens ATPase, H ⁺ -transporting, lysosomal (vacuolar proton pump) 16kD (ATP8C) mRNA
1371	6368	11417	1.13	8.0E-39	4758229	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EPBAG9) mRNA
1783	6784		1.43	8.0E-39	AB23404.1	EST_HUMAN	wh53f10_x1_NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR-P87890 P87890 POL PROTEIN;
2038	7021	12130	4.22	7.0E-39	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
992	6005	11036	1.95	5.0E-39	AF003528.1	NT	Homo sapiens X-linked emphydrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2816	7935	12933	6.76	5.0E-39	AI750154.1	EST_HUMAN	al36f04_x1_Bartfelder colon HPLB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR-Q15408
546	6580	10584	50.63	4.0E-39	AB015810.1	NT	Q15408 NEUTRAL PROTEASE LARGE SUBUNIT contains LTR7.11 LTR7 repetitive element;
3492	8500	13514	0.7	4.0E-39	AL163210.2	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
48	5129	10121	18.3	3.0E-39	AA631949.1	EST_HUMAN	HS21C010
48	5129	01222	18.3	3.0E-39	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
48	5129	10123	18.3	3.0E-39	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
888	5904		18.94	2.0E-39	BE408203.1	EST_HUMAN	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
901	5919		8.24	2.0E-39	AI525119.1	EST_HUMAN	pronmine-7.D01.1 rat brain mRNA Homo sapiens cDNA 6'
1016	6029		3.1	2.0E-39	AF003573.1	NT	Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds
1498	6496		89.79	2.0E-39	AW372318.1	EST_HUMAN	PM0-B10340-211289-003-012 BT0340 Homo sapiens cDNA
1929	6915	12012	2.58	2.0E-39	AA720574.1	EST_HUMAN	nm21902_s1_NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.i3
2558	7521	12638	1.41	2.0E-39	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4279	9272	14261	1.83	2.0E-39	BF310207.1	EST_HUMAN	RC4-FN0031-28070-01-e10 FN0037 Homo sapiens cDNA
1482	6479	11535	11.08	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene

Page 94 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1482	6479	11536	11.08	1.0E-39	AJ006345.1	NT	Human sapiens <i>KV1QT1</i> gene
1489	6497	11650	4.37	1.0E-39	7657020	NT	Human sapiens DKK2p434p221 protein (DKF2p434p221), mRNA
4525	9515	14500	15.01	1.0E-39	AW851895.1	EST_HUMAN	EST364065 MAGE resequences, MAGB Homo sapiens cDNA
4525	9515	14501	15.01	1.0E-39	AW851895.1	EST_HUMAN	EST364065 MAGE resequences, MAGB Homo sapiens cDNA
4584	8552	14538	7.93	1.0E-39	7657020	NT	Human sapiens DKK2p434p221 protein (DKF2p434p221), mRNA
551	5585	10587	1.74	9.0E-40	5803210	NT	Human sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1215	6214	11263	11.93	8.0E-40	4765145	NT	Human sapiens AE-binding protein 1 (AEBP1) mRNA
1215	6214	11254	11.93	9.0E-40	4755145	NT	Human sapiens AE-binding protein 1 (AEBP1) mRNA
1423	6420	11480	1.06	9.0E-40	4507512	NT	Human sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudodinflammatory) (TIMP3), mRNA
3697	8701	13704	1.19	8.0E-40	4503764	NT	Human sapiens fragile X mental retardation 1 (FMR1) mRNA
3866	10048	13870	3.4	9.0E-40	AB033070.1	NT	Human sapiens mRNA for KIAA1244 protein, partial cds
4370	8214	14183	0.88	9.0E-40	4507848	NT	Human sapiens ubiquitin specific protease 13 (Isopeptidase T-3) (USP13) mRNA
2868	7886	13000	0.96	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H15A04
3823	8825	4.81	8.0E-40	BE398541.1	EST_HUMAN	601288958FTNIH_MGC_8_Homo sapiens cDNA clone IMAGE:361B166 5'	
2854	7814	12724	6.7	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2529	7495	12615	6.7	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
1838	6828	11917	1.77	4.0E-40	AI686005.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR-O73605_O73506
2050	7032		2.06	4.0E-40	AF003328.1	NT	Human sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4284	9267	14247	8.89	4.0E-40	7682117	NT	Human sapiens KIAA0433 protein (KIAA0433), mRNA
4011	9007	13986	0.89	3.0E-40	AI925949.1	EST_HUMAN	wh12601_x1_NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2350549 3'
323	5377		3.68	2.0E-40	AI223036.1	EST_HUMAN	q952h08_x1_Soares_Jestis_NH-T Homo sapiens cDNA clone IMAGE:1838847 3'
788	5807		47.86	2.0E-40	AV303886.1	EST_HUMAN	xx24e10_x1_NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW_RS5_MOUSE_P97461_40S_RIBOSOMAL PROTEIN S5.;
1790	6781		2.37	2.0E-40	AV731601.1	EST_HUMAN	AV731601_HFF_Homo sapiens cDNA clone HTFAZE06 5'
1894	6882	11973	6.41	2.0E-40	4508188	NT	Human sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSM7) mRNA, and translated products
1894	6882	11974	6.41	2.0E-40	4508188	NT	Human sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSM7) mRNA, and translated products

Page 95 of 209
Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2105	7085	12200	1.63	2.0E-40	5453562	NT	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA
2818	7580	13080	1.3	2.0E-40	B0276532.1	EST_HUMAN	6011215677F_NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
3053	8070	14717	4.08	2.0E-40	5453562	NT	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA
4745	9730	14718	1.8	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4745	9730	14718	1.8	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5005	9976	14951	1	2.0E-40	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
872	5890	12831	1.42	1.0E-40	AA225389.1	EST_HUMAN	nc09405_s1_NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:1007608
2548	7613	12831	1.42	1.0E-40	B07036881.1	EST_HUMAN	601460375F_NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863863 5'
2614	7576		1.6	1.0E-40	BE018348.1	EST_HUMAN	bb79a10.y1_NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z168 Q9Z158
2863	7622	12733	0.89	1.0E-40	BF541030.1	EST_HUMAN	6020686504F_NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067738 5'
2863	7622	12734	0.89	1.0E-40	BF541030.1	EST_HUMAN	6020686504F_NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067738 5'
3224	8239		1.22	1.0E-40	4507142	NT	Homo sapiens sorting neitin 3 (SNX3) mRNA
4478	94688		5.47	1.0E-40	4508012	NT	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
3715	8718	13720	1.02	9.0E-41	W01698.1	EST_HUMAN	za36a02.1_Scares fetal liver spleen 1NFL5 Homo sapiens cDNA clone IMAGE:284602 5'
818	7732	10874	1.8	7.0E-41	AI934384.1	EST_HUMAN	wp04h04.x1_NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
818	7732	10875	1.8	7.0E-41	AI934384.1	EST_HUMAN	wp04h04.x1_NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
5041	10012	14981	1.23	7.0E-41	11431114	NT	Homo sapiens hypothetical protein (FLJ0996), mRNA
278	5336	10350	2.15	8.0E-41	AB037163.1	NT	Homo sapiens DSCR6b mRNA, complete cds
2052	7034	12148	4.09	8.0E-41	7657012	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1766	6758	11844	1.57	5.0E-41	T62628.1	EST_HUMAN	yc03e10.s1_Stratagene lung (#837210)-Homo sapiens cDNA clone IMAGE:786283
360	5428		1.45	4.0E-41	BE156318.1	EST_HUMAN	QV0-HT0367150200-114-939 HT0367 Homo sapiens cDNA
1081	6088	11117	1.03	4.0E-41	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
1385	6382	11432	10.1	4.0E-41	A027117.1	EST_HUMAN	ow4506.s1_Scares_parathyroid_tumor_NbHPA_Homo sapiens cDNA clone IMAGE:1649784 3' similar to TR:O00597_O00597_CYTOKHROME_C-LIKE POLYPEPTIDE ;contains LTR5 repetitive element;
1385	6382	11433	10.1	4.0E-41	A1027117.1	EST_HUMAN	ow4506.s1_Scares_parathyroid_tumor_NbHPA_Homo sapiens cDNA clone IMAGE:1649784 3' similar to TR:O00597_O00597_CYTOKHROME_C-LIKE POLYPEPTIDE ;contains LTR5 repetitive element;
1398	6395	11450	3.73	4.0E-41	AB008681.1	NT	Homo sapiens gene for actinin receptor type IIb, complete cds
1595	6591						Im86c04.x1_NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2168958 3' similar to contains OFR.b1
2818	7838	12854	4.42	4.0E-41	A1500406.1	EST_HUMAN	OFR repetitive element.
2818	7838	12855	3.89	4.0E-41	AJ228041.1	NT	Homo sapiens B59 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2818	7838	12856	3.89	4.0E-41	AJ228041.1	NT	Homo sapiens B59 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4021	9017	14004	2.21	4.0E-41	X92685.1	NT	H.sapiens DNase I hypersensitive site (HSS-3) enhancer element
833	5950	10983	1.82	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
4208	9201	14183	3.05	3.0E-41	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 112 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1789	6827	11586	48.39	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
1918	6804	11988	1.61	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week (Homo sapiens cDNA 5' end)
2157	7136	12256	5.84	2.0E-41	D86962.1	NT	Human mRNA for KIAA0207 gene, complete cds
2208	7183	12306	15.51	2.0E-41	X89631.1	NT	G. gorilla DNA for ZNF80 gene homolog
2755	6827	11586	16.52	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3748	8752	13761	0.8	2.0E-41	5032106.1	NT	Homo sapiens son of sevens (Drosophila) homolog 1 (SOS1) mRNA
4488	8478	14458	1.15	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4488	9478	14459	1.15	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3133	8149	13170	1.16	1.0E-41	BE859735.1	EST_HUMAN	[601445647/F1_NIH_MGC_65] Homo sapiens cDNA clone IMAGE:3849803 5'
3133	8149	13171	1.16	1.0E-41	BE859735.1	EST_HUMAN	[601445647/F1_NIH_MGC_65] Homo sapiens cDNA clone IMAGE:3849803 5'
4434	9424	14409	15.18	1.0E-41	6678468.1	NT	Mus musculus tubulin alpha 3 (Tub36), mRNA
460	5497	10508	6.2	8.0E-42	AF003550.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
4976	9952	14930	0.94	8.0E-42	66789031.1	NT	Mus musculus neural precursor cell expressed, developmentally down-regulated gene 1 (Nedd1), mRNA
919	5935		1.72	7.0E-42	AL163295.2	NT	Homo sapiens chromosome 21 segment HS21C085
1818	6809	11900	3.13	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (PI4K230) mRNA, complete cds
1818	6809	11901	3.13	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (PI4K230) mRNA, complete cds
2227	7204		2.79	6.0E-42	AW238656.1	EST_HUMAN	xP29f05.x1 NCI CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741798 3' similar to contains L1.11 L1 repetitive element ;
136	5202		5.47	5.0E-42	AJ271735.1	NT	Homo sapiens Xq pseudodautosomal region; segment 1/2
435	5473	10489	1.36	5.0E-42	BE271913.1	EST_HUMAN	Inv31e11.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175362 3'
483	5520		8.24	5.0E-42	5730038.1	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
484	6521		3.56	5.0E-42	5730038.1	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
744	8767	10792	23.3	4.0E-42	AF050566.1	NT	Homo sapiens MHC class 1 region
744	6767	10783	23.3	4.0E-42	AF050566.1	NT	Homo sapiens MHC class 1 region
1049	6056	11087	4.34	4.0E-42	AF18801.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4071	8065	14055	1.98	4.0E-42	X58417.1	NT	H.sapiens PRKC27 mRNA
4106	8100	14087	0.92	4.0E-42	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4127	9122	14101	4.17	4.0E-42	4500498.1	NT	Homo sapiens regulatory factor X-4 (influences HLA class II expression) (REFX4) mRNA
4451	9441	14422	13.19	4.0E-42	4508008.1	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA

Page 97 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
104	6181		0.9	3.0E-42	AA486105.1	EST_HUMAN	abi14e10_s1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR_12 THR repetitive element;
1452	6449	11510	2.61	2.0E-42	BF768834.1	EST_HUMAN	RC0-TN0079-1-10900-024-807 TN0079 Homo sapiens cDNA
2346	7320		2.82	2.0E-42	AW888344.1	EST_HUMAN	RC3-NN0070-270400-011-h110 NN0070 Homo sapiens cDNA
2358	7332	12448	4.89	2.0E-42	AW800589.1	EST_HUMAN	2B19283.3 prime NIH MGC_7 Homo sapiens cDNA clone IMAGE:2B19283 3'
724	5746	10767	2.18	1.0E-42	X57147.1	NT	Human endogenous retrovirus PHE_1 (ERV8)
1025	6035	11087	1.09	1.0E-42	AW285809.1	EST_HUMAN	Ui-H-B11-afh-0-04-0-Ui_S1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1084	6091	11120	1.08	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1084	6091	11121	1.08	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1223	7742	11287	11.85	1.0E-42	AF067168.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1223	7742	11288	11.95	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1661	6687	—11731	1.13	1.0E-42	11123219	NT	Homo sapiens tec (LOC51201), mRNA
2473	7442	12557	1.26	1.0E-42	5174468	NT	Homo sapiens major histocompatibility complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
2894	7913	12834	5.85	1.0E-42	4505524	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3626	8633	13638	2.28	1.0E-42	7662027	NT	Homo sapiens Golgi vesicular membrane trafficking protein p18 (BET1) mRNA
3705	8709	13712	0.82	1.0E-42	5031610	NT	Homo sapiens chromosome 21 segment HS21C087
3825	8827	13834	1.03	1.0E-42	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C080
4124	9119	14105	1.89	1.0E-42	AL163280.2	NT	RC3-ST0197-161098-012-e03 ST0197 Homo sapiens cDNA
4462	9452	14433	0.75	1.0E-42	AW813617.1	EST_HUMAN	Homo sapiens proteasome inhibitor (P31), mRNA
4602	9590	14577	2.94	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (P31), mRNA
4602	9590	14578	2.94	1.0E-42	5803122	NT	Homo sapiens tyrosine receptor 3 (RYR3) mRNA
4634	9819	14811	5.64	1.0E-42	45056758	NT	AV736824 CB Homo sapiens cDNA clone CBLAKH108 5'
644	5872	10876	12.63	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH108 5'
644	5872	10877	12.63	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH108 5'
691	5715	10729	6.28	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
691	5715	10730	5.28	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
691	5715	10731	5.28	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
3556	8563	13569	8.21	7.0E-43	AW248442.1	EST_HUMAN	2B22251.5 prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2B22251 5'
1324	6322		24.68	6.0E-43	AA491890.1	EST_HUMAN	nt72dd08_e1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909803 similar to qbl056085 60S RIBOSOMAL PROTEIN L30 (HUMAN);
2516	7484		2.96	6.0E-43	AV708201.1	EST_HUMAN	AV708201 ADC Homo sapiens cDNA clone ADCACCTG 5'

Page 98 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
142	5208		1.98	5.0E-43	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
489	6535	10541	3.04	5.0E-43	AA382780.1	EST_HUMAN	EST186033 Testis 1 Homo sapiens cDNA 5' and 3' EST
2773	7784	12814	1.82	5.0E-43	AV732578	HTFF_Homo sapiens cDNA clone HTFANC08 5'	Homo sapiens X-linked ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
958	7698	11007	5.71	4.0E-43	AF003528.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1194	6198		3.19	3.0E-43	AF223391.1	NT	Homo sapiens gene encoding La autoantigen
1656	6832	11724	4.45	3.0E-43	X07889.1	NT	AML1-EVI-1=AML1-EVI-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA (mRNA), 3938 nt]
3491	8499	13513	1.29	3.0E-43	SS6902.1	EST_HUMAN	cd81c09_x1 Soares testis cDNA clone IMAGE:1017419
4187	9162	14148	0.69	3.0E-43	AA548164.1	EST_HUMAN	cd81c09_x1 Soares testis cDNA clone IMAGE:1733988 3' similar to contains PTR7.3 PTR7 PTR7 repetitive element;
183	5246		21.1	2.0E-43	AI190764.1	EST_HUMAN	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1810	6606	11659	2.07	1.0E-43	AF154838.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1610	6606	11870	2.07	1.0E-43	AF154838.1	NT	Homo sapiens chromosome 21 segment HS21C084
1668	6662	11737	1.71	1.0E-43	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2652	7612	12722	4.87	1.0E-43	BF548231.1	EST_HUMAN	BF548231.1 Homo sapiens cDNA clone IMAGE:4157866 5'
878	5897	10938	4.62	8.0E-44	AI222985.1	EST_HUMAN	AI222985.1 Homo sapiens cDNA clone IMAGE:1845552 3'
878	5897	10939	4.62	8.0E-44	AI222985.1	EST_HUMAN	AI222985.1 Homo sapiens cDNA clone IMAGE:1845552 3'
4721	9706	14692	1.2	8.0E-44	AW373186.1	EST_HUMAN	RC5-BT0503-081289-011-9122 BT0503 Homo sapiens cDNA
4721	9706	14693	1.2	8.0E-44	AW373185.1	EST_HUMAN	RC5-BT0503-081289-011-9122 BT0503 Homo sapiens cDNA
651	5879	6651	1.08	7.0E-44	RO5035.1	EST_HUMAN	ye83601_x1 Soares fetal liver spleen 1NF/S Homo sapiens cDNA clone IMAGE:124920 5'
2172	7151	12270	1.31	7.0E-44	5031888.1	NT	Homo sapiens LIM domain-containing protein partner in lipoma (LPP) mRNA
2886	7915	12835	2.47	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
2886	7915	12836	2.47	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3772	8775	13779	2.74	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4119	9113	14098	1.21	7.0E-44	AF231018.1	NT	Homo sapiens chromosome 21 unknown mRNA
4119	9113	14099	1.21	7.0E-44	AF231019.1	NT	Homo sapiens chromosome 21 unknown mRNA
301	5358		3.07	5.0E-44	AJ289860.1	NT	Homo sapiens KIAA0851 gene (partial), X73 gene and LZTFL1 gene
330	6382		1.86	5.0E-44	AJ289860.1	NT	Homo sapiens KIAA0851 gene (partial), X73 gene and LZTFL1 gene
3330	8340	13358	3.08	4.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4854	8835		1.24	4.0E-44	AI435225.1	EST_HUMAN	AI435225.1 Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNAG) mRNA
1748	8742		1.97	3.0E-44	6912477	NT	Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNAG) mRNA
2460	7429	12546	1.98	3.0E-44	BE880628.1	EST_HUMAN	BE880628.1 Homo sapiens cDNA clone IMAGE:3883839 5'

Page 99 of 209

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3024	8041	13050	6.08	3.0E-44	AA168851.1	EST_HUMAN	zp18b05_r1 Strategene fetal retina clone IMAGE:609777 5'
1032	6042	11071	2.58	2.0E-44	4826885	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1032	6042	11072	2.58	2.0E-44	4826885	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1189	6189	11228	4.87	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TM21) mRNA
1188	6189	11227	4.87	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TM21) mRNA
1293	6291	11337	4.09	2.0E-44	AF135888.1	NT	Homo sapiens RAB36 (RAB36) mRNA, complete cds
1351	6348	11398	1.58	2.0E-44	BE465325.1	EST_HUMAN	hcv4g08_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182838 3' similar to SW-0XYB_HUMAN
2091	7072	12186	2.43	2.0E-44	AF070851.1	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
2536	7501		3.54	2.0E-44	5901833	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
3390	8398	13424	1.87	2.0E-44	D87675.1	NT	Homo sapiens DNA for emyloid precursor protein, complete cds
4437	8427	14411	1.65	2.0E-44	AW884376.1	EST_HUMAN	PM4-SN0016-120500-003-004 SN0016 Homo sapiens cDNA
4644	8629	14623	1.01	2.0E-44	7708128	NT	Homo sapiens oxysterol 7alpha-hydroxylase (CYP39A1) mRNA
4644	8829	14624	1.01	2.0E-44	7708128	NT	Homo sapiens oxysterol 7alpha-hydroxylase (CYP39A1) mRNA
53	5134	10130	8.52	1.0E-44	7657334	NT	Homo sapiens Misspliced/ILK-related kinase (MILNK), mRNA
53	5134	10131	8.52	1.0E-44	7657334	NT	Homo sapiens Misspliced/ILK-related kinase (MILNK), mRNA
575	6607	10606	1.72	1.0E-44	AW851132.1	EST_HUMAN	RC1-CT0249-030300-026-112 C70248 Homo sapiens cDNA
1178	6180		1.29	1.0E-44	AW894803.1	EST_HUMAN	RC1-BN00398-110300-012-001 BN00398 Homo sapiens cDNA
1539	6557		3.98	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2163	7142	12259	3.27	1.0E-44	AA434554.1	EST_HUMAN	zv53dd02_r1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to
2163	7142	12260	3.27	1.0E-44	AA434554.1	EST_HUMAN	zv53dd02_r1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to
							Homo sapiens THR-13 THR repetitive element;
2685	7643	12758	1.28	1.0E-44	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, JM6 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
3642	8648		4.21	1.0E-44	AA465869.1	EST_HUMAN	ba01c09_s1 Scores_NHMPU_S1 Homo sapiens cDNA clone IMAGE:811984 3'
4945	8922	14900	0.76	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
4445	9435	14418	1.81	1.0E-45	8922381	NT	Homo sapiens alpha satellite DNA, M1 monomer type
4445	9435	14419	1.61	1.0E-45	8922381	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379) mRNA
2453	7423	12538	4.1	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
4910	9889	14852	8.47	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
2887	7806		1.91	7.0E-45	AL160131.1	NT	Novel human gene mapping to chromosome 22

Page 100 of 209
Table 4

Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1621	6518			1.01	6.0E-45 AI675425.1	EST_HUMAN	WB88cd6.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2313802 3' similar to contains L1.11 L1 repetitive element;
3871	8872			9.19	6.0E-45 AW157570.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782890 3' similar to SW_R13A_HUMAN_P40429_60S_RIBOSOMAL_PROTEIN_L13A ;
881	5899			1.17	5.0E-45 AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1856	6942	12044		2.41	5.0E-45 BF333627.1	EST_HUMAN	CM4-CN0044-180200-516-01 CN0044 Homo sapiens cDNA clone IMAGE:2118453 3' similar to SW_PAX1_MOUSE
3137	8153	13176		2.09	5.0E-45 AI625768.1	EST_HUMAN	tg84f07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2118453 3' similar to SW_PAX1_MOUSE
1126	6131	11161		13.11	4.0E-45 X98828.1	NT	P08084 PAIRED BOX PROTEIN PAX-1. ;
2229	7206	12321		3.69	4.0E-45 BE265822.1	EST_HUMAN	H.sapiens ART4 gene
3946	8944	13934		1.07	4.0E-45 4503422	NT	60119444051 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3638425 5'
3256	8269			1.58	3.0E-45 T71480.1	EST_HUMAN	Homo sapiens dUTP pyrophosphatase (DUT) mRNA
3871	8269			1.78	3.0E-45 T71480.1	EST_HUMAN	yd35f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
2429	7400			1.54	2.0E-45 AI163218.2	NT	yd35f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
2982	7880	12984		1.28	2.0E-45 AI1243213.1	NT	Homo sapiens chromosome 21 segment HS21C018
124	5443			3.37	1.0E-45 BE389856.1	EST_HUMAN	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
406	5443			3.74	1.0E-45 BE389855.1	EST_HUMAN	601284360F NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606163 5'
469	5505	10519		1.3	1.0E-45 45064412	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1155	6159	11193		1.76	1.0E-45 7687280	NT	Homo sapiens Langerhans cell specific c-type leucin (LANGERIN), mRNA
3030	8047	13057		7.83	1.0E-45 U32168.1	NT	Human pro-α2 chain of collagen type XI (COL11A2) gene, complete cds
3412	8421	13450		0.79	1.0E-45 86589568	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
4350	9341	14322		4.49	1.0E-45 BE396633.1	EST_HUMAN	601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619803 5'
2374	7348	12466		26.07	8.0E-46 AI433261.1	EST_HUMAN	B3208.x1 NCI_CGAP_Gata4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_rna2
2374	7348	12467		28.07	8.0E-46 AI433261.1	EST_HUMAN	TUBULIN_BETA-1 CHAIN (HUMAN);
2177	7156	12276		1.08	7.0E-46 U46007.1	NT	Rattus norvegicus espin mRNA, complete cds
4447	9437			8.98	7.0E-46 BE386166.1	EST_HUMAN	601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
4662	9647			1.73	7.0E-46 BE064386.1	EST_HUMAN	RC4-BT0310-110306-015-f010_B10310 Homo sapiens cDNA
2681	7839	12754		3.59	6.0E-46 AI884381.1	EST_HUMAN	wm31f08.x1 NCI_CGAP_U44 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.2
2681	7839	12755		3.59	6.0E-46 AI884381.1	EST_HUMAN	MER19 repetitive element;
204	5268			4.44	5.0E-46 AL163210.2	NT	wm31f08.x1 NCI_CGAP_U44 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.2
							Homo sapiens chromosome 21 segment HS21C010

Page 101 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3450	8468	13484	1.07	5.0E-46	BE877194.1	EST_HUMAN	7db1f01_x1 Lipski_dorsal root_ganglion Homo sapiens cDNA clone IMAGE:3279400 3'
3450	8468	13485	1.07	5.0E-46	BE877194.1	EST_HUMAN	7db1f01_x1 Lipski_dorsal root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
635	5663		2.5	4.0E-46	AA801143.1	EST_HUMAN	ncs4e09_s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104620 3' similar to gb:X53741_ma1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1665	6661	11735	8.01	4.0E-46	AW770544.1	EST_HUMAN	h186c03_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element;
1665	6681	11736	8.01	4.0E-46	AW770544.1	EST_HUMAN	h186c03_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element;
2688	7625	12737	2.58	4.0E-46	M18048.1	NT	Human endogenous retrovirus RTVL-H2
4283	9285	14272	0.97	4.0E-46	AB014522.1	NT	Hom sapiens mRNA for KIAA0822 protein, partial cds
4283	9285	14273	0.97	4.0E-46	AB014522.1	NT	Hom sapiens mRNA for KIAA0822 protein, partial cds
2222	7189	12319	1.23	3.0E-46	7657203	NT	Hom sapiens acidic 82 kDa protein mRNA (HSU15552), mRNA
2361	7335	12452	2.18	3.0E-46	AF06212.1	NT	Hom sapiens VAMP-associated 33 kDa protein mRNA, complete cds
4269	9292	14252	0.72	3.0E-46	4506376	NT	Hom sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4630	9615	14605	1.22	3.0E-46	Z73660.1	NT	H.sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; Vlambda
4630	9815	14606	1.22	3.0E-46	Z73660.1	NT	H.sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; Vlambda
827	5847	10884	8.39	2.0E-46	AA168646.1	EST_HUMAN	ne05a09_s1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:3800408 3' similar to contens THR-b2 THR repetitive element;
1601	6597	11658	2.53	2.0E-46	U78027.1	NT	Hom sapiens Bruton's tyrosine kinase (BTK), alpha-D-selectostidase A (GLA), L44-like ribosomal protein (L44L) and F1P3 (F1P3) genes, complete cds
4815	9789	14780	1.31	2.0E-46	AA399288.1	EST_HUMAN	Q01730 RSP-1 PROTEIN ;
1213	6212	11252	5.7	1.0E-46	4502694	NT	Hom sapiens cell division cycle 10 (homologous to CDC10 of <i>S. cerevisiae</i>) (CDC10) mRNA
1538	6538	11594	1.27	1.0E-46	7662177	NT	Hom sapiens KIAA0555 gene product (KIAA0555), mRNA
1538	6536	11695	1.27	1.0E-46	7662177	NT	Hom sapiens KIAA0555 gene product (KIAA0555), mRNA
2218	7195	12317	3.81	1.0E-46	AW978516.1	EST_HUMAN	EST3806255 MAGE resequences, MAGP Homo sapiens cDNA
2336	7310	12431	2.62	1.0E-46	H97330.1	EST_HUMAN	EST485095 WATM1 Homo sapiens cDNA clone 485095
3176	8182	13213	8.47	1.0E-46	AA851912.1	EST_HUMAN	np78802_s1 NCI_CGAP_P72 Homo sapiens cDNA clone IMAGE:1132385 similar to gb:X76717 H.sapiens MT-11 mRNA, (HUMAN);
4723	9703		3	1.0E-46	AB023197.1	NT	Hom sapiens mRNA for KIAA0980 protein, partial cds

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
757	5778		3.81	9.0E-47	AJ271735.1	NT	Homo sapiens Xq pseudodautosomal region; segment 11/2
4776	9760	14747	2.41	9.0E-47	AW770928.1	EST_HUMAN	h183e04.x1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008534 3' similar to TR:O75703 O75703
1772	6784	11852	90.6	8.0E-47	Y18538.1	NT	Homo sapiens HLA-C gene, exon 5, Individual 18323
1772	6784	11853	90.6	8.0E-47	Y18538.1	NT	Homo sapiens HLA-C gene, exon 6, Individual 18323
2644	7804	12717	1.38	8.0E-47	5453955	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
2857	7976	12891	1.73	8.0E-47	AJ228043.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21;q22, segment 3/3
2477	7446	12859	1.23	6.0E-47	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1378	6373	11423	5.93	4.0E-47	4557556	NT	Homo sapiens chromosome 21 segment HS21C046
540	6575	10580	3.84	3.0E-47	BE907634.1	EST_HUMAN	6011497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3889721 5'
640	6575	10581	3.84	3.0E-47	BE907634.1	EST_HUMAN	6011497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3889721 5'
808	5829	10860	4.98	3.0E-47	N57483.1	EST_HUMAN	6011497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3889721 5'
931	5948	10982	7.81	3.0E-47	AL163284.2	NT	Y55b04.s1 Soares multiple sclerosis cDNA clone IMAGE:3889721 5'
3230	8245	13287	0.84	3.0E-47	4504116	NT	Homo sapiens chromosome 21 segment HS21C084
3859	8861		6.7	3.0E-47	U93181.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4237	8231	14214	1.25	3.0E-47	M12859.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SBP1) mRNA, partial cds
147	5213	10227	1.29	2.0E-47	4505318	NT	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
953	5969	11001	2.67	2.0E-47	AL163209.2	NT	Homo sapiens phosphatase, target subunit 2 (MTP12) mRNA
953	5969	11002	2.67	2.0E-47	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
1558	6555	11816	2	2.0E-47	7682109	NT	Homo sapiens chromosome 21 segment HS21C009
1638	6635	11705	3.76	2.0E-47	AA524514.1	EST_HUMAN	Homo sapiens KIAA0426 gene product (KIAA0426) mRNA
4221	9215	14194	1.6	2.0E-47	4504668	NT	hg43h12.s1 NC1 CGAP_C03 Homo sapiens cDNA clone IMAGE:937607 3'
4229	9253	14240	1.82	2.0E-47	AA568592.1	EST_HUMAN	Homo sapiens ring finger protein (C3HC4 type) B (RNFB) mRNA
4229	9253	14241	1.82	2.0E-47	AA568592.1	EST_HUMAN	inf23g07.s1 NC1 CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
4376	9367	14347	2.23	2.0E-47	5176448	NT	Homo sapiens Rev/Rex activation domain binding protein-related (FABP_R) mRNA
4687	9862	14640	1.32	2.0E-47	AW86566.1	EST_HUMAN	EST377239 IMAGE sequences, MAGI Homo sapiens cDNA
1381	6378	11428	4.13	1.0E-47	A133429.1	EST_HUMAN	Q9BH03.x1 Soares, fetal lung, NbHL19W Homo sapiens cDNA clone IMAGE:1831189 3'
3731	8735	13732	2.17	1.0E-47	BE280477.1	EST_HUMAN	601166321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 6'
3731	8735	13733	2.17	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
4904	9883	14854	3.23	1.0E-47	AW813906.1	EST_HUMAN	FC3_S70197-130400-017-012 ST0197 Homo sapiens cDNA
1575	6572	11653	3.85	9.0E-48	AT223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-9, and partial cds, alternatively spliced
1231	6230		1.49	8.0E-48	4501980	NT	Homo sapiens amidinylate 1 (ACY1) mRNA

Page 103 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1232	6230			8.0E-48	4501800	NT	Homo sapiens aminopeptidase 1 (ACY1), mRNA hk61b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to qb:X84707
3082	8079	13092		3.91	8.0E-48	AW768477.1	EST_HUMAN BREAST BASIC CONSERVED PROTEIN 1 (HUMAN); hk61b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to qb:X84707
3062	8079	13093		3.91	8.0E-48	AW768477.1	EST_HUMAN BREAST BASIC CONSERVED PROTEIN 1 (HUMAN); hk61b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to qb:X84707
487	5524			1.31	7.0E-48	AB035035.1	NT
488	5524			19.03	7.0E-48	AB035035.1	NT
1467	6484	11623		1.05	7.0E-48	6912719	NT
1597	6593	11654		6.73	7.0E-48	6730038	NT
3518	8526	13537		7.99	6.0E-48	AI761111.1	EST_HUMAN wf69n03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398613 3'
3237	10046	13272		1.61	5.0E-48	4826891	NT
1831	6917	12016		28.02	3.0E-48	4885170	NT
1831	6917	12016		28.02	3.0E-48	4885170	NT
4125	9120			0.89	3.0E-48	AA009541.1	EST_HUMAN Z04603.r1 Scares, fetal liver, spleen, 1NFLS, S1 Homo sapiens cDNA clone IMAGE:429844 5'
5	6086	10071		1.14	2.0E-48	AA465007.1	EST_HUMAN Z80c03.r1 Scares, fetal liver, spleen, 1NFLS, S1 Homo sapiens cDNA clone IMAGE:810052 5'
46	5127	10118		2.18	2.0E-48	AA4631840.1	EST_HUMAN fmf67 Regional genomic DNA specific cDNA library, Homo sapiens cDNA library, Human-HGSC project, TCBAP/D3842 Pediatric pre-B cell acute lymphoblastic leukemia, Baylor-HGSC project, TCBAP/D3842 Pediatric pre-B cell acute lymphoblastic leukemia, Baylor-HGSC project, TCBAP/D3842
4401	8392	14376		0.95	2.0E-48	BE246065.1	EST_HUMAN FB2E2_Fetal brain, Strategene Homo sapiens cDNA clone FB2E2_3 end
4803	9787	14768		1.1	2.0E-48	T03176.1	EST_HUMAN FB2E2_Fetal brain, Strategene Homo sapiens cDNA clone FB2E2_3 end
4803	9787	14770		1.1	2.0E-48	T03176.1	EST_HUMAN FB2E2_Fetal brain, Strategene Homo sapiens cDNA clone FB2E2_3 end
5064	10033	15000		1.11	2.0E-48	AW470877.1	EST_HUMAN xm67a10.x1 NCI_CG6_Homo sapiens cDNA clone IMAGE:28689242 3'
57	5137	10135		8.01	1.0E-48	7706534	NT
862	5881	10922		4.37	1.0E-48	4502166	NT
1059	6068	11088		3.2	1.0E-48	7657430	NT
1059	6068	11089		3.2	1.0E-48	7657430	NT
1277	6278	11317		4.07	1.0E-48	5032032	NT
1874	6863	11952		15.16	1.0E-48	AL163302.2	NT
3408	8417	13445		1.25	1.0E-48	AL163246.2	NT
4959	6936	11914		0.91	1.0E-48	M10976.1	NT
1959	6945	12047		0.92	8.0E-49	AB026497.1	NT
139	5430	10445		4.24	7.0E-49	5729890	NT
139	6430	10446		4.24	7.0E-49	5729890	NT
392	5430	10445		3.24	7.0E-49	5729890	NT

Page 104 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
392	5430	10446	3.24	7.0E-49	5729890	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
393	5430	10445	2.69	7.0E-49	5729890	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
393	6430	10446	2.89	7.0E-49	5729890	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1201	6202	11239	3.59	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
							be55005_x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800504 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
197	5281	10274	180.31	6.0E-49	AW731740.1	EST_HUMAN	
1340	6338	11387	0.98	6.0E-49	BF038268.1	EST_HUMAN	601457738F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3861272 5'
1340	6338	11386	0.99	6.0E-49	BF038269.1	EST_HUMAN	601457738F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3861272 5'
3989	8985	13983	0.88	6.0E-49	AL162091.1	EST_HUMAN	DKFZp761A138_51 761 (synonym: hanyp2) Homo sapiens cDNA clone DKFZp761A138 3'
702	5728	10741	7.26	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
702	5728	10742	7.26	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
							zp28e07.11 Stratagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:610860 5' similar to TR:G233228 G233228 RTVL-H PROTEIN ;contains LTR7_LTR7 repetitive element ;
1758	8751	11385	3.85	5.0E-49	AA172121.1	EST_HUMAN	
2677	7635	12750	7.57	5.0E-49	U17714.1	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
3199	8215	13236	8.74	5.0E-49	114363355	NT	
							Homo sapiens similar to ribosomal protein S27 (metallopanstimulin 1) (H. sapiens) (LOC83362) mRNA
621	5556	10558	22.88	4.0E-49	AW186533.1	EST_HUMAN	x08b01_x1 NCI_CGAP_UK Homo sapiens cDNA clone IMAGE:2876593 3' similar to WP:80350_2B
556	5590	10591	0.9	3.0E-49	X88986.1	NT	H.sapiens mRNA for acetyl-CoA carboxylase
2575	7538		1.21	3.0E-49	AA016131.1	EST_HUMAN	za31c05_r1 Scales retina N2b4HR Homo sapiens cDNA clone IMAGE:3860584 5' similar to contains L1.13 L1 repetitive element;
4824	8803	14780	2.5	3.0E-49	U46899.1	NT	Human type IV collagen (COL4A1) gene, exon 40
4899	9970		0.94	3.0E-49	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
653	5881		3.08	2.0E-49	BE165980.1	EST_HUMAN	MF3-H70487-150200-113-901 HT0487 Homo sapiens cDNA
3151	8167	13187	1.44	2.0E-49	N28446.1	EST_HUMAN	yc23d08_r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:2822571 5'
888	5906		6.86	1.0E-49	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862066 5'
1522	6519	11576	27.09	1.0E-49	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1765	6757	11843	5.52	1.0E-49	BE255216.1	EST_HUMAN	601115769F NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356273 6'
169	6234	10244	2.76	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
709	6733	10749	1.82	8.0E-50	X85097.2	NT	Homo sapiens mRNA for VIP receptor 2
709	5753	10750	1.82	8.0E-50	X85097.2	NT	Homo sapiens mRNA for VIP receptor 2
1726	6721	11758	13.5	8.0E-50	4501880	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA

Page 105 of 209

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2411	7382	12600	1.29	8.0E-50	7706394	NT	Human sapiens P47 (LOC51674), mRNA
2411	7382	12501	1.29	8.0E-50	7706394	NT	Human sapiens P47 (LOC51674), mRNA
2827	7587	12689	3.51	8.0E-50	4826658	NT	Human sapiens capping protein (elc1n filament) muscle Z-line, beta (CAPZB), mRNA
4217	9210		0.88	6.0E-50	BE794381.1	EST_HUMAN	601569565F11 NIH_MGC_7_Homo sapiens cDNA clone IMAGE:3943577 6'
1757	8750	11833	1.19	5.0E-50	BF332938.1	EST_HUMAN	CM0-BT0792-300500-398-b05_BT0782_Homo sapiens cDNA
1757	8750	11834	1.19	5.0E-50	BF332938.1	EST_HUMAN	CM0-BT0792-300500-398-b05_BT0782_Homo sapiens cDNA
906	5923		1.83	4.0E-50	AA801143.1	EST_HUMAN	hg54609_s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_ma1
3365	8373	13383	0.98	4.0E-50	AL163248.2	NT	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1898	6886		2.31	3.0E-50	M18648.1	NT	Human sapiens chromosome 21 segment HS21C048
2447	7417	12532	1.05	3.0E-50	BE259186.1	EST_HUMAN	601109777F11 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350309 6'
3225	8240	13282	0.89	3.0E-50	AA746142.1	EST_HUMAN	ob03f08_s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322627 3'
							hg26e01_s1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2948744 3' similar to SW-C1TC_HUMAN
5032	10003	14974	1.04	3.0E-50	AW582886.1	EST_HUMAN	P11588_C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;contains Alu repetitive element
769	5780		14.02	2.0E-50	AF055086.1	NT	Human sapiens MHC class 1 region
1063	6071	11103	5.6	2.0E-50	4557752	NT	Human sapiens midline 1 (OplizBBB syndrome) (MID1) mRNA
1417	6414	11475	1.29	2.0E-50	AF138303.1	NT	Human sapiens decorin D mRNA, complete cds, alternatively spliced
3214	8228	13250	0.78	2.0E-50	AF11168.2	NT	Human sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
4138	9133	14116	1.11	2.0E-50	D88424.1	NT	Mus musculus mRNA for high-sulfur keratin protein, partial cds
459	6496	10507	1.74	1.0E-50	AL163209.2	NT	Human sapiens chromosome 21 segment HS21C009
2304	7278		7.62	1.0E-50	AL1271735.1	NT	Human sapiens Xq pseudoautosomal region; segment 1/2
4435	9425	14410	12.15	8.0E-51	AA810842.1	EST_HUMAN	hp38e08_s1 NCI_CGAP_Lu11 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:X12671_ma1
2850	7869	2898	1.33	7.0E-51	AW274720.1	EST_HUMAN	hr34_s03_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:28955684 3' similar to TR-Q9Z340
3209	8224	13246	1.63	7.0E-51	AW889218.1	EST_HUMAN	Q92340-NT0028-200400-180-d05 NT0028 Homo sapiens cDNA
							hr34a03_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:28955684 3' similar to TR-Q9Z340
3282	8284	13319	0.82	7.0E-51	AW274720.1	EST_HUMAN	Q92340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
4043	9039	14029	1.26	7.0E-51	AL078628.1	EST_HUMAN	DKFZp434B2228_r1_434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434B2228 6'
4043	9039	14030	1.25	7.0E-51	AL078628.1	EST_HUMAN	DKFZp434B2228_r1_434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434B2228 5'
4225	9219	14198	2.54	7.0E-51	AW285603.1	EST_HUMAN	U1-H-BW0-sip-b-05-c-U_1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2728817 3'
1498	6494	1549	1.16	6.0E-51	6678763	NT	Human sapiens putative DNA binding protein (M98), mRNA

Page 106 of 209

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1934	6920	12019	3.34	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
3393	8401	134227	15.79	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
783	5804	10334	5.86	5.0E-51	AL162203.2	NT	Homo sapiens chromosome 21 segment HS21C003
794	5815	10346	1.74	6.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
978	7738	11024	1.07	6.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1571	6558	11630	1.42	5.0E-61	6031980	NT	Homo sapiens 28S rRNA-associated p41 homolog (POH1) mRNA
2517	7485	12601	8.01	5.0E-61	AJ007656.1	NT	Homo sapiens mRNA for nucleoporin 155
3841	8843	13550	3.87	5.0E-61	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
3841	8843	13851	3.67	6.0E-61	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4900	8878	14848	1.54	5.0E-61	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
135	5201	10217	20.61	3.0E-51	AL687348.1	EST_HUMAN	tr81cd9_x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1157	6161	11195	35.84	3.0E-51	AL587348.1	EST_HUMAN	tr81cd9_x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1882	6871	11860	1.08	3.0E-51	AA211298.1	EST_HUMAN	zg87901_s1 Strategene hnt neuron (#937233) Homo sapiens cDNA clone IMAGE:849008 3'
4220	9193	14176	2.01	3.0E-51	AL159112.1	NT	Novel human gene mapping to chromosome 22
365	5414	10427	2.45	2.0E-51	4507788	NT	Homo sapiens ubiquitin protein ligase E3R (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
678	5704	10712	1.65	2.0E-51	BE391063.1	EST_HUMAN	601265694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
679	5704	10713	1.85	2.0E-51	BE391063.1	EST_HUMAN	601265694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
1649	6645	11718	6.36	2.0E-51	AA233352.1	EST_HUMAN	zr30a05_r1 Strategene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:869880 5' similar to TR-G23226 G23226 RTV-H PROTEIN, contains LTR7.13 LTR repetitive element;
3848	8654	136860	2.94	2.0E-51	AL492415.1	EST_HUMAN	zr27603_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3'
114	5186	10195	45.03	1.0E-51	4503528	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
1462	6459	5124	1.0E-51	AV742248.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone GBFBCC12 5'	
151	5217	10230	7.75	8.0E-52	AA72054.1	EST_HUMAN	nw21602_s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:12411138 3' similar to contains THR13 THR repetitive element;
1466	6463	11622	1.35	8.0E-52	XB4900.1	NT	H.sapiens mRNA for laminin-5, alpha3b chain
1614	6610	11674	2.31	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1614	6610	11675	2.31	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA

Page 107 of 209
Table 4
Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLASTE Value	Top Hit No.	Top Hit Accession	Top Hit Database Source	Top Hit Descriptor
3888	6810	11674	6.2	8.0E-52	11988028	NT		Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3888	6610	11675	6.2	8.0E-52	11988028	NT		Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1655	6651	11723	3.39	6.0E-52	AF08807.1	NT		Homo sapiens hypothetical protein S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4318	9310	14298	2.8	5.0E-52	Z78888.1	NT		H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pa18H7
1622	6619	11685	1.32	4.0E-52	AF257318.1	NT		Homo sapiens SH3-containing protein SH3GL1B1 mRNA, complete cds
1750	6744	11823	2.08	4.0E-52	4758843	NT		Homo sapiens nucleoprotein 155D (NUP155) mRNA
3826	8828	13835	0.81	4.0E-52	4507500	NT		Homo sapiens T-cell lymphoma invasion and metastasis 1 (Tiam1) mRNA
4514	8504	14484	1.26	4.0E-52	5174550	NT		Homo sapiens 5,10-methylentetrahydrofolate dehydrogenase, 5,10-methylentetrahydrofolate synthetase, 10-formyltetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase (MTHFD) mRNA
3975	8973	1025	3.0E-52	11437042	NT			Homo sapiens hypothetical protein FLJ10675 (FLJ10675) mRNA
658	6592	10592	1.85	2.0E-52	M10976.1	NT		Human endogenous retroviral DNA (4-1), complete retroviral segment
558	6592	10593	1.85	2.0E-52	M10976.1	NT		Human endogenous retroviral DNA (4-1), complete retroviral segment
1718	8713	11780	1.15	2.0E-52	AB007898.1	NT		Homo sapiens mRNA for KIAA1249 protein, partial cds
1984	6949	12052	1	2.0E-52	AB033075.1	NT		Homo sapiens mRNA for KIAA1249 protein, partial cds
2428	7397	12518	3.12	2.0E-52	BE207575.1	EST_HUMAN		bb6807_y1_NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gB:XI6463 M.musculus mRNA for Zfp121 zinc finger protein (MOUSE);
2662	7821		19.48	2.0E-52	BF677892.1	EST_HUMAN		602084710F1_NIH_MGC_83 Homo sapiens cDNA clone IMAGE:1248891 5'
4818	8802	14782	3.17	2.0E-52	AL137188.3	NT		Novel human gene mapping to chromosome 20, similar to membrane transporters
4853	9834	14808	1.1	2.0E-52	AI141802.1	EST_HUMAN	q566e05_s1_Sources_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1680784 3'	
4853	9834	14809	1.1	2.0E-52	AI141802.1	EST_HUMAN	q566e05_s1_Sources_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1680784 3'	
529	5584	10368	1.37	1.0E-52	AA63445.1	EST_HUMAN		z175h12_s1_Sources_NIH Homo sapiens cDNA clone IMAGE:743879 3'
1354	6351	11401	9.59	1.0E-52	4504026	NT		Homo sapiens glutamate-ammonia lyase D (ARSD), transcript variant 1, mRNA
2465	7434		1.67	1.0E-52	4502238	NT		Homo sapiens glutamate-aminosulfatase (GLUL) mRNA
2985	8003	13015	1.99	1.0E-52	S61070.1	NT		pol=reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element R7VL-Hp1, Genomic, 660 nt]
3702	8706	13708	1.3	9.0E-53	4506064	NT		Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
4267	9260	14250	1.22	8.0E-53	AF001446.1	NT		Homo sapiens core binding factor alpha1 subunit (CBF1) gene, exon 3
5033	10004	14975	1.19	8.0E-53	AB040937.1	NT		Homo sapiens mRNA for KIAA1604 protein, partial cds
3982	6980	139865	15.99	5.0E-53	4756643	NT		Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
50	5131	10125	1.53	4.0E-53	AL163285.2	NT		Homo sapiens chromosome 21 segment HS21C055
50	5131	10126	1.53	4.0E-53	AL163285.2	NT		Homo sapiens chromosome 21 segment HS21C085

Page 108 of 209

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4675	8660	14643	0.88	4.0E-53	7705414 NT	Homo sapiens hook1 protein (HOOK1), mRNA	
2569	7652	12667	1.47	3.0E-53	AB026898.1	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	w22c07_x1 Soares, Dieckgraef, coon, NHCD Homo sapiens cDNA clone IMAGE:2558788 3'
3647	8653	13659	1.94	3.0E-53	AW050836.1	EST_HUMAN	IL2-UM0081-240300-455-D03 UM0081 Homo sapiens cDNA
4457	9447	14427	0.73	3.0E-53	AW050563.1	EST_HUMAN	EST77625 Pancreas tumor III Homo sapiens cDNA 5' end
455	5492		3.68	2.0E-53	AA366568.1	EST_HUMAN	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-selectosidase A (GLA), L44-like ribosomal protein (L44L) and FIP3 (FTP3) genes, complete cds
2266	7243	12360	20.13	2.0E-53	U78027.1	NT	Homo sapiens A TPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar protein-ATPase, subunit E; V-ATPase, subunit E (ATP5E), mRNA
2466	7435		7.48	2.0E-53	4502316 NT	Homo sapiens leucine aminopeptidase (LC551056), mRNA	
3147	8163	13183	0.92	2.0E-53	7705687 NT	Homo sapiens dihydroxyidole receptor alpha 2 subunit (CACNA2D1) gene, exon 6	
3172	8188	13210	2.53	2.0E-53	AF083822.1	EST_HUMAN	Human Kruppel-related DNA-binding protein (TF34) gene, partial cds
3947	8945	13835	2.5	2.0E-53	M61873.1	EST_HUMAN	Homo sapiens SKAP55 homolog (SKAP-HOM) mRNA
4365	9358	14336	0.92	2.0E-53	4506982 NT	Homo sapiens Xg pseudatosomal region; segment 2/2	
1420	6417	11477	1.56	1.0E-53	A1277738.1	NT	Homo sapiens Xg pseudatosomal region; segment 2/2
3325	8335	13355	1.23	1.0E-53	AB026898.1	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	
4807	9781	14773	1.54	1.0E-53	BE296886.1	EST_HUMAN	EST1176725F1 NIH MGC_117 Homo sapiens cDNA clone IMAGE:3531919 5'
6039	10010	14979	0.97	1.0E-53	AW957429.1	EST_HUMAN	EST369619 MAGE gene sequences, Homo sapiens cDNA
207	5271	10283	4.09	8.0E-54	BE386785.1	EST_HUMAN	6012728653F1 NIH MGC_20 Homo sapiens cDNA clone IMAGE:3814031 5'
1789	6790	11880	2.71	8.0E-54	4504610 NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA	
4696	8384	14573	0.71	8.0E-54	4507848 NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA	
4598	8584	14574	0.71	8.0E-54	4507848 NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA	
383	5458	10476	1.58	7.0E-54	AA812537.1	EST_HUMAN	ai79c12_s1 Soares, NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30,13 MER30 repetitive element;
1794	6785	11875	1.37	7.0E-54	Y168465.1	NT	Homo sapiens mRNA for monocyte chemoattractant protein-2
2142	7121	12237	4.24	7.0E-54	N27177.1	EST_HUMAN	yw68d12_s1 Soares, placenta, 81cweeks_2NbHP81c9W Homo sapiens cDNA clone IMAGE:257399 3'
5043	10014	14983	1.08	7.0E-54	AI276750.1	EST_HUMAN	similar to contains LTR7_b3 LTR7 repetitive element;
23	5103	10088	6.96	6.0E-54	AB003618.1	NT	q164610_x1 Soares, NIHMP, S1 Homo sapiens cDNA clone IMAGE:19777130 3'
384	5459	10478	1.73	6.0E-54	8922148 NT	Homo sapiens DNA for M1CB, exon 4, 5 and partial cds	
384	5459	10477	1.73	6.0E-54	8922148 NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA	
3210	8225	12247	2.1	6.0E-54	8922148 NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA	
3898	8898	13898	1.11	6.0E-54	4502872 NT	Homo sapiens chloride channel 6 (CLCN6), mRNA	

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor	
4696	9681	14864	1.19	6.0E-54	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA	
4724	9709		2.36	6.0E-54	Y0946.1	NT	H. sapiens stc pseudogene, p68 isoform	
4841	9709		2.18	6.0E-54	Y0946.1	NT	H. sapiens stc pseudogene, p68 isoform	
2050	7071	12185		3.25	5.0E-54	P51623	SWISSPROT ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)	
182	5245		283.62	4.0E-54	AF110103.1	NT	Tupula belangen hetero-actin mRNA, partial cds	
941	5958	10991	140.55	4.0E-54	AA308784.1	EST_HUMAN	EST177698 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase	
1769	6761	11848	2.65	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds	
1769	6761	11849	2.55	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds	
3131	8147		1.39	4.0E-54	AI935088.1	EST_HUMAN	wd26411.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:Q02711 O02711 PRO-POL-DUTAPE POLYPROTEIN;	
92	5169	10179	30.76	3.0E-54	AA313487.1	EST_HUMAN	EST1853371 Soares_NFL_T_GBC_S1 Homo sapiens cDNA 5' end	
2651	7516		1.04	3.0E-54	AI908757.1	EST_HUMAN	IL-BT189-180389-007 BT189 Homo sapiens cDNA	
636	5684	10688	6.13	2.0E-54	5031800	NT	Homo sapiens killer cell lectin-like receptor subunit G, member 1 (KLRG1) mRNA	
1347	6344	11395	2.11	2.0E-54	4507164	NT	Homo sapiens nuclear antigen Sp100 (SP100) mRNA	
1515	6513	11569	1.19	2.0E-54	AA855008.1	EST_HUMAN	nt78a09.s1 NCI_CGAP_P13 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element;	
2469	7437	12554	1.47	2.0E-54	AW163175.1	EST_HUMAN	au9203.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783784 5' similar to SW-CU1_HUMAN Q13618 CULLIN HOMOLOG 1;	
2524	7480	12610	1.65	2.0E-54	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010	
2824	7845	12865	1.51	2.0E-54	AW057524.1	EST_HUMAN	wy60b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to TR:Q62084 C62084 PHOSPHOLIPASE C NEIGHBORING:	
3472	8480		7.32	2.0E-54	AA53225.1	EST_HUMAN	nt4509.s1 NCI_CGAP_P18 Homo sapiens cDNA clone IMAGE:995488 similar to sbX53777 60S RIBOSOMAL PROTEIN L23 (HUMAN);	
4082	8076		3.11	2.0E-54	4502842	NT	Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA	
4319	8311		1.14	2.0E-54	AF208161.1	NT	Homo sapiens synapsin precursor, mRNA, complete cds	
5052	10023	14992	0.92	2.0E-54	4506962	NT	Homo sapiens SHAP65 homologue (SHAP-HOM) mRNA	
4341	9332		1.35	1.0E-54	BF315418.1	EST_HUMAN	601899230f1.NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'	
1298	6226		1.8	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein	
1065	6073	11106	1.85	7.0E-55	RO9346.1	EST_HUMAN	Y28e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127898 5' similar to SP_C561_BOVIN P10897 CYTOCHROME;	
1733	6728	11804		2.5	6.0E-55	AA704971.1	EST_HUMAN	795b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462817 3'
1733	6728	11805		2.5	6.0E-55	AA704971.1	EST_HUMAN	295b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462817 3'
4626	9811	14600		1.31	5.0E-55	AW206021.1	EST_HUMAN	U1-H-B11-81y-8-09-0-U1 s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723538 3'

Page 110 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
58	7712	10134	6.49	4.0E-55	AW857884.1	EST_HUMAN	EST137064 MAGE ressequences, MAGE Homo sapiens cDNA
684	5680	10689	29.4	4.0E-55	4826973 NT	Homo sapiens RNA binding motif, Y chromosome, family 1, member A1 (RBMY1A1) mRNA	
1414	6412	11471	1.58	4.0E-55	7861713 NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA	
1414	6412	11472	1.58	4.0E-55	7861713 NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA	
1483	6480		1.43	4.0E-55	BFO61411.1	EST_HUMAN	752b10.x1 Scores, NSF_F8_8W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE3386049 3' similar to contains L1 L1 repetitive element;
1974	6959	12064	1.95	4.0E-55	4506180 NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA	
1974	6959	12055	1.95	4.0E-55	4506180 NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA	
2032	7015	12123	3.3	4.0E-55	4503314 NT	Homo sapiens diacylglycerol kinase, gamma (80kD) (DGKG) mRNA	
2032	7015	12124	3.3	4.0E-55	4503314 NT	Homo sapiens diacylglycerol kinase, gamma (80kD) (DGKG) mRNA	
2247	7224	12344	4.51	4.0E-55	4507784 NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA	
3206	8221	13243	1.2	4.0E-55	AL163300.2 NT	Homo sapiens chromosome 21 segment HS21C100	
4985	9959	14938	2.08	4.0E-55	BE698871.1	EST_HUMAN	RC2-U70023-280700-011-f03 U70023 Homo sapiens cDNA
376	6423	10438	2	2.0E-55	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
547	6581		1.08	2.0E-55	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
641	5689	10673	4.78	2.0E-55	4507286 NT	Homo sapiens syntaxin-binding protein 1 (STXBP1) mRNA, and translated products	
2889	7808	12929	1.7	2.0E-55	4507798 NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA	
4629	8614	14804	2.97	2.0E-55	BE719886.1	EST_HUMAN	CM1-H10876-150800-357-103 HT0876 Homo sapiens cDNA
85	6112	0192	2.86	1.0E-55	4505050 NT	Homo sapiens mannosidase-3-phosphate receptor (cation dependent) (M6PR) mRNA	
189	6253	10284	113.02	1.0E-55	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Refelbia2) mRNA, complete cds
569	5802	10600	14.24	1.0E-55	A1028718.1	EST_HUMAN	ov59g8_x1 Scores testis NT Homo sapiens cDNA clone IMAGE1844160 3'
1132	6137	11198	6.88	1.0E-55	AB022010.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
1911	6897	11891	6	1.0E-55	BE277381.1	EST_HUMAN	601120116F NIH_MGC_20 Homo sapiens cDNA clone IMAGE2987027 5'
1911	6897	11932	5	1.0E-55	BE277381.1	EST_HUMAN	601120116F NIH_MGC_20 Homo sapiens cDNA clone IMAGE2987027 5'
2263	7240		6.39	1.0E-55	5803174 NT	Homo sapiens SMAS (SMAS) mRNA	
2446	7416	12531	63.73	1.0E-55	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2483	7451	125684	3.06	1.0E-55	AB007886.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2483	7451	125685	3.08	1.0E-55	AB007886.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2539	7503	126222	14.65	1.0E-55	L54057.1	NT	Homo sapiens CLP mRNA, partial cds
2717	7674	12787	0.88	1.0E-55	AB033045.1	NT	Homo sapiens mRNA for KIAA1219 protein, partial cds
3389	8397	13422	1.83	1.0E-55	5174590 NT	Homo sapiens 5,10-methylenetetrahydrofolate dehydrogenase, 5,10-methylenetetrahydrofolate cyclohydrase, 10-formyltetrahydrofolate synthetase (MTHFD) mRNA	

Page 111 of 209

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3389 8397	13423	1.83	1.0E-55	5174590	NT	[Homo sapiens 5,10-methylentetrahydrofolate dehydrogenase, 5,10-methylenetetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase (MTHFD) mRNA	
3883 8884	13882	3.86	1.0E-55	AL1632387.2	NT	Homo sapiens chromosome 21 segment HS21C067	
4170 9185	14192	1.64	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010	
4592 9580		1.01	1.0E-55	NT77261.1	EST_HUMAN	yy44g03.r1 Seires fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2255620 6'	
4858 9835	14913	1.08	1.0E-55	8923125	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA	
6015 9898	14982	2.2	1.0E-55	BE077188.1	EST_HUMAN	RC3-BT0565-150200-031-B11 BT0605 Homo sapiens cDNA	
2659 7819	12730	3.83	7.0E-56	H168844.1	EST_HUMAN	yr62g03.r1 Seires adult brain N2b5hIB56Y Homo sapiens cDNA clone IMAGE:173044 6' similar to contains THR repetitive element;	
1653 6849	11721	1.83	5.0E-58	AW887712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA	
28 5108	10082	44.14	4.0E-58	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds	
28 5108	10093	44.14	4.0E-58	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds	
2636 7598	12709	7.3	4.0E-58	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA	
2838 7598	12710	7.3	4.0E-58	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA	
2740 5557	10560	3.58	4.0E-58	AF00328.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	
1322 6320	11368	3.78	3.0E-58	8924029	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA	
1727 6722	11800	3.22	3.0E-58	6912743	NT	Homo sapiens 6'-3' exoribonuclease 2 (XRN2), mRNA	
2089 7070	12184	1.19	3.0E-58	6912697	NT	Homo sapiens oncogene TC21 (TC21), mRNA	
3052 8069	13078	1.47	3.0E-58	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end	
3052 8069	13079	1.47	3.0E-58	AA325828.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end	
3745 8749		2.03	3.0E-58	AF055068.1	NT	Homo sapiens MHC class I region	
3818 8820	13827	1.28	3.0E-58	BE38312.1	EST_HUMAN	603102035F-1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631848 5'	
4263 9256	14246	1.91	3.0E-58	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA	
4300 8292	14279	4.75	3.0E-58	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068	
4440 9430	14414	2.24	3.0E-58	5902055	NT	Homo sapiens superkiller viral acidic activity 2 (S. cerevisiae homolog) like (SKIV2L), mRNA	
4941 9918	14898	0.72	3.0E-58	6912593	NT	Homo sapiens phosphotidylinositol transfer protein, beta (PTTPNB), mRNA	
4984 9918	14898	0.83	3.0E-58	6912593	NT	Homo sapiens phosphotidylinositol transfer protein, beta (PTTPNB), mRNA	
520 5555		1.87	2.0E-58	AA198918.1	EST_HUMAN	zq52a08.s1 Strategene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:646206 3'	
723 7729	10765	1.67	2.0E-58	BE064886.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA	
723 7729	10766	1.67	2.0E-58	BE064886.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA	
2321 7286	12416	0.94	2.0E-58	IM28061.1	NT	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds	
2321 7286	12417	0.94	2.0E-58	IM28061.1	NT	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds	
2919 7838	12955	1.04	2.0E-58	AB0317835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds	

Page 112 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3242	8225			1.89	2.0E-56 AB008881.1	NT	Homo sapiens gene for actinin receptor type II B, complete cds
3456	8464	13191		1.29	2.0E-56 AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBeFG10 5'
665	6980			4.42	1.0E-56 AF180930.1	NT	Macaca fasciularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
1489	8486	11541		2.19	1.0E-56 AA283038.1	EST_HUMAN	254b09.1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:726137 5' similar to gb:MG4654
3590	8597	13501		2.28	1.0E-56 AW589833.1	EST_HUMAN	INTERLEUKIN ENHANCER-BINDING FACTOR (HUMAN); hg23c11.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2916452 3'
3590	8597	13502		2.28	1.0E-56 AW589833.1	EST_HUMAN	hg23c11.x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:2916452 3'
620	6647			1.82	9.0E-57 AW880985.1	EST_HUMAN	QVO-OT0033-070306-152-h03 O70033 Homo sapiens cDNA
4081	8075	14063		0.97	9.0E-57	4758279 NT	Homo sapiens EphA4 (EPHA4) mRNA
4081	9075	14064		0.97	9.0E-57	4758279 NT	Homo sapiens EphA4 (EPHA4) mRNA
295	5352	10365		2.81	8.0E-57 AW816405.1	EST_HUMAN	QV4-ST0234-181189-037405 ST0234 Homo sapiens cDNA
873	5891	10932		7.02	8.0E-57 AW264599.1	EST_HUMAN	x05d10.21 NCI CGAP_Bns3 Homo sapiens cDNA clone IMAGE:27159251 3' similar to gb:U05875
1780	6772	11684		1.69	8.0E-57 AA498108.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN); zv51b12.1 Soares testis NH1 Homo sapiens cDNA clone IMAGE:757151 5'
3287	8308	13333		1.37	8.0E-57	4758279 NT	Homo sapiens EphA4 (EPHA4) mRNA
3287	8308	13334		1.37	8.0E-57	4758279 NT	Homo sapiens EphA4 (EPHA4) mRNA
4869	9849	14825		0.81	8.0E-57 BE289916.1	EST_HUMAN	600Ba4440F1 NIH MGC_17 Homo sapiens cDNA clone IMAGE:28608864 5'
2561	7525	12842		0.97	7.0E-57	7657592 NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2561	7625	12843		0.97	7.0E-57	7657592 NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
3177	8193	13214		1.16	7.0E-57	7242168 NT	Homo sapiens NME7 (NME7), mRNA
3177	8193	13215		1.16	7.0E-57	7242158 NT	Homo sapiens NME7 (NME7), mRNA
3187	8213	13235		0.74	7.0E-57	6005979 NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3786	8789	13783		2.1	7.0E-57 AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pI4K230) mRNA, complete cds
3786	8789	13794		2.1	7.0E-57 AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pI4K230) mRNA, complete cds
4308	8300			1.78	7.0E-57 AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3668	8673	13677		2.42	4.0E-57 AB028698.1	NT	Homo sapiens DNA, DLEC1 to ORC1L3, ORC1L4 genes, complete cds
795	5816	10847		1.62	3.0E-57	4607798 NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1311	6308			163.33	3.0E-57 AA230279.1	EST_HUMAN	nc1307.81 NCI CGAP_Pri Homo sapiens cDNA clone IMAGE:1008037 similar to SW.RST0_HUMAN
2327	7301	12421		1.31	3.0E-57 AA348335.1	EST_HUMAN	P46783 40S RIBOSOMAL PROTEIN S10.; EST54770 Hippocampus II Homo sapiens cDNA 5' end

Page 113 of 209

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2631 7691	12703	1.45	3.0E-57	BE676622.1	EST_HUMAN	7f33b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3298443 3' similar to WP:Y47HBC:2 CE20263 ;	
2631 7591	12704	1.45	3.0E-57	BE676622.1	EST_HUMAN	7f33b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3298443 3' similar to WP:Y47HBC:2 CE20263 ;	
3482 8490	13568	1.73	3.0E-57	AF232708.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein (CCh) gene, complete cds	
3614 8621		31.12	3.0E-57	AW859884.1	EST_HUMAN	RC3-C10254-110300-027-410 CT0254 Homo sapiens cDNA	
1471 6488	11528	1.55	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds	
1471 6498	11527	1.55	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds	
2337 7311	12432	1.04	2.0E-57	BE72826.1	EST_HUMAN	MR0-HT0559-010400-0098-H10 HT0559 Homo sapiens cDNA	
3354 8382		3.62	2.0E-57	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004	
3474 8492	13561	0.68	2.0E-57	RD7702.1	EST_HUMAN	ye98h01.r1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'	
3474 8482	13562	0.68	2.0E-57	RD7702.1	EST_HUMAN	ye98h01.r1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'	
3828 8830	13837	0.83	2.0E-57	BE073284.1	EST_HUMAN	MR0-BT0551-060300-103-b03 BT0551 Homo sapiens cDNA	
4063 8057	14044	1.05	2.0E-57	AA0110298.1	EST_HUMAN	za00c06.1 Scares retina N2b4-HR Homo sapiens cDNA clone IMAGE:381450 5'	
4063 9057	14045	1.05	2.0E-57	AA0110298.1	EST_HUMAN	za00c06.1 Scares retina N2b4-HR Homo sapiens cDNA clone IMAGE:381450 5'	
4379 9370	14349	8.08	2.0E-57	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C083	
2170 7149	12266	1.48	1.0E-57	AW503208.1	EST_HUMAN	U1-HF-BND-akt-g-07-0-U1.NI NIH MGC_50 Homo sapiens cDNA clone IMAGE:3073348 5'	
584 5615		1.9	8.0E-58	BE863715.1	EST_HUMAN	601445948F1 NIH MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'	
646 5674	10879	4.07	8.0E-58	AI788376.1	EST_HUMAN	It34b07.x1 NCI_CGAP_O23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;	
646 5674	10880	4.07	8.0E-58	AI798376.1	EST_HUMAN	It34b07.x1 NCI_CGAP_O23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;	
1820 6810	11802	1.74	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA	
1820 6810	11803	1.74	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA	
2808 7825		2.79	8.0E-58	7706132	NT	Homo sapiens DHHC1 protein (LOC51304), mRNA	
2192 7171	12292	0.98	6.0E-58	BE398061.1	EST_HUMAN	601309468F1 NIH MGC_44 Homo sapiens cDNA clone IMAGE:3831000 5'	
2314 7289	12410	10.37	6.0E-58	AU130689.1	EST_HUMAN	AU130689 N12RP3 Homo sapiens cDNA clone N12RP3001263 5'	
2831 7851	12870	0.94	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baytar-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219	
2831 7851	12871	0.94	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baytar-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219	
288 5355	10367	3.24	5.0E-58	4507334	NT	Homo sapiens synaptosomal (SYN1), mRNA	
700 5724	10740	6.5	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-160800-018-b05 NT0057 Homo sapiens cDNA	
1175 6178	11213	3.64	5.0E-58	AW797048.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA	

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1175	6178	11214	3.84	5.0E-58	AW797848.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1176	6178	11213	2.81	5.0E-58	AW797848.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1176	6178	11214	2.81	5.0E-58	AW797848.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3249	8262	13283	8.16	5.0E-58	AA988183.1	EST_HUMAN	or98e07_st1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603908 3'
4136	9131	14114	0.98	5.0E-58	AI6381745.1	EST_HUMAN	1s85e07_x1 NCI_CGAP_Gc8 Homo sapiens cDNA clone IMAGE:2233468 3' similar to SW:PRO2_ACACA_P19984_PROFILIN II ;
372	5421	10435	8.26	4.0E-58	4502302 NT		Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O) mRNA
788	5809	10839	1.73	4.0E-58	4504834 NT		Homo sapiens interleukin 10 receptor, beta (IL10RB) mRNA
1440	6437	11494	1.06	4.0E-58	4503848 NT		Homo sapiens coagulation factor IX (plasma thromboplastin component, Christmas disease, hemophilia B) (F9) mRNA
2559	7524	12840	2.19	4.0E-58	U36251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3655	8661	13666	1.09	4.0E-58	50316860 NT		Homo sapiens EGFR-like repeats and discoidin I-like domains 3 (EDIL3) mRNA
333	5385		1.23	3.0E-58	R17879.1	EST_HUMAN	Yg10e02_r1 Soares infant brain 1NIH Homo sapiens cDNA clone IMAGE:31693 5'
1366	6363	14142	1.88	3.0E-58	47569881 NT		Homo sapiens peptide YY (PYY) mRNA
3105	8121	13138	3.33	3.0E-58	BF569789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308943 5'		602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308943 5'
3105	8121	13139	3.33	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308943 5'
926	6943	10977	7.87	2.0E-58	AF068824.1	NT	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds
							RIBOSOMAL PROTEIN L6 (HUMAN); gb:x81987 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
1271	6269		27.01	2.0E-58	BE208532.1	EST_HUMAN	be08b07_v1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X69391 60S
712	5738	10752	0.84	1.0E-58	M65134.1	NT	Human complement component C5 mRNA, 3' end
1051	6060	11089	9.81	1.0E-58	6274549 NT		Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22D, B22) (NDUFB9) mRNA
1307	6305	11352	1.04	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGE resequences, MAGD Homo sapiens cDNA
1307	6305	11353	1.04	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGE resequences, MAGD Homo sapiens cDNA
1373	6370	11419	3.35	1.0E-58	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1624	6621	11689	1.46	1.0E-58	BE468132.1	EST_HUMAN	hy10f08_x1 NCI_CGAP_G66 Homo sapiens cDNA clone IMAGE:3189935 3'
2582	7645	12659	0.66	1.0E-58	AF217514.1	NT	Homo sapiens uncharacterized bone marrow protein Bm038 mRNA, complete cds
2730	7687	12801	1.98	1.0E-58	4759169 NT		Homo sapiens sterol regulatory element binding transcription factor 2 (SREEF2) mRNA
4811	9795	14778	5.68	1.0E-58	A114103.1	EST_HUMAN	czz43h01_x1 Soares_NhIMMu_S1 Homo sapiens cDNA clone IMAGE:1678128 3'
2168	7147	12284	69.17	8.0E-59	4507378 NT		Homo sapiens TATA box binding protein (TBP) mRNA
177	7714		2.98	6.0E-59	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862088 5'

Page 115 of 209
Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1715	6710	11786	9.16	5.0E-59	AW157281.1	EST_HUMAN	au83h05_x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to TR:075786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
1715	6710	11787	9.16	5.0E-59	AW167281.1	EST_HUMAN	au83h05_x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to TR:075786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
3054	8071	13081	6.88	5.0E-59	AI807484.1	EST_HUMAN	wf48c11_x1 Spears, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358838 3'
4523	9513	14498	9.33	5.0E-59	>X38497.1	NT	H.sapiens DNA for ZNF80-linked ERVb long terminal repeat
785	5806	10837	2.84	4.0E-59	DB00068.1	NT	Human mRNA for KIAA0184 gene, partial cds
1218	6217	11258	0.87	4.0E-59	4506618	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1218	6217	11259	0.67	4.0E-59	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
5017	8988	14894	0.96	4.0E-59	AI890347.1	EST_HUMAN	ws32612_x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2438928 3'
10	5090		4.74	3.0E-59	AW1665524.1	EST_HUMAN	EST377582 MAGE sequences, MAG1_Homo sapiens cDNA
225	5287	10295	4.43	3.0E-59	7662247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
1612	6688	11743	8.3	3.0E-59	4505860	NT	Homo sapiens plasmoringer activator, tissue (PLATE) mRNA
1612	6688	11744	8.3	3.0E-59	4505860	NT	Homo sapiens plasmoringer activator, tissue (PLATE) mRNA
2071	7053	12162	5.59	3.0E-59	AB029036.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2071	7053	12163	6.59	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2897	7779	12769	0.98	3.0E-59	AF232289.1	NT	Homo sapiens NF1-2 pseudogene, exon 17
3056	8073	13085	3.67	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3056	8073	13086	3.67	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3735	8739	13738	1.33	3.0E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4547	9536	14523	1.09	3.0E-59	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4693	9678	14682	1.64	3.0E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type T (PTPRT), mRNA
4884	9863		0.92	3.0E-59	M95681.1	NT	Human prohormone converting enzyme (NEC2) gene, exon 2
182	5228		37.68	1.0E-59	BE286411.1	EST_HUMAN	601176757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531827 5'
2644	7509		2.32	1.0E-59	AA748468.1	EST_HUMAN	Q13537 MER37 TRANSPOSSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
754	5776	10803	2.17	8.0E-60	AW977845.1	EST_HUMAN	ca56h11_st NCL_CGAP_GC61 Homo sapiens cDNA clone IMAGE:1305029 3' similar to TR:Q13537
1443	6440	11497	8.32	8.0E-60	4759169	NT	EST369849 MAGE sequences, MAGO_Homo sapiens cDNA
2107	7087	12201	1.59	8.0E-60	5174656	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRNPD3) mRNA
2107	7087	12202	1.59	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
746	5768	10794	33.65	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region
746	5768	10794	108.11	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region

Page 116 of 209

Table 4
Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
805	6926	108566	1.3	7.0E-60	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
2070	7052	12161	1.23	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds	
2712	7669	12782	0.98	7.0E-60	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
4055	9049	14037	4.26	7.0E-60	4505488	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
2114	7094	12208	1.15	6.0E-60	BE9B4974.2	EST_HUMAN	601658751R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:38818068 3'
82	5159	10169	0.98	5.0E-60	AI807917.1	EST_HUMAN	wf52c07_x1_Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
82	5159	10170	0.98	5.0E-60	AI807917.1	EST_HUMAN	wf52c07_x1_Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2173	7152	12271	1.15	4.0E-60	AW503208.1	EST_HUMAN	U1-HF-BND-4kt-g-07-0-U1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2173	7152	12272	1.15	4.0E-60	AW503208.1	EST_HUMAN	U1-HF-BND-4kt-g-07-0-U1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2803	7922	1.51	4.0E-60	AA2899037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol	
1822	6812	11805	3.27	3.0E-60	BE562811.1	EST_HUMAN	601358446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:36901385 5'
1822	6812	11808	3.27	3.0E-60	BE562811.1	EST_HUMAN	601358446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:36901385 5'
1832	6822	8.77	3.0E-60	6031180	NT	Homo sapiens prothrombin (PTB) mRNA	
4335	8326	14311	1.67	3.0E-60	AJ271735.1	NT	Homo sapiens Xq pseudosatosomal region; segment 1/2
31	5111	10097	1.22	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1399	6396	11461	6.78	2.0E-60	Z11694.1	NT	H_sapiens_41kDa protein kinase related to rat ERK2
1683	6679	11752	1.46	2.0E-60	M24603.1	NT	Human bcr protein mRNA, 5' end
1692	6868	11763	1.24	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
2532	7487	12617	1.04	2.0E-60	7857229	NT	Homo sapiens interleukin 17 receptor (IL17R) mRNA
3498	8508	13521	0.82	2.0E-60	4757867	NT	Homo sapiens v-faf murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
3817	8819	13928	0.8	2.0E-60	AF231819.1	NT	Homo sapiens chromosome 21 unknown mRNA
518	5553	10556	1	1.0E-60	BE7886.1	EST_HUMAN	PM3-HT0505-270200-001-006 HT0805 Homo sapiens cDNA AU148389 Y78AA1001854 5'
3806	8809	13815	1.97	1.0E-60	AI143389.1	EST_HUMAN	Hom sapiens cDNA clone 21 segment HS21C085
4789	9783	14768	1.67	1.0E-60	AI163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1082	6089	11118	2.32	9.0E-61	AU118344	EST_HUMAN	AU118344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
2699	7581	12678	1.72	8.0E-61	AV008478.1	EST_HUMAN	wf05b10_x1_NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2806595 3'
2569	7581	12878	1.72	8.0E-61	AV008478.1	EST_HUMAN	wf05b10_x1_NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2806595 3'
2880	7899	2.34	8.0E-61	X57147.1	NT	Human endogenous retrovirus pHE_1 (ERV9)	
128	5195	10209	1.8	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
128	5195	10210	1.8	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
4923	5195	10209	2.82	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
4923	5195	10210	2.92	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA

Page 117 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
263	5322	10334	4.42	8.0E-61	BE409310.1	EST_HUMAN	601300938F_NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
802	5823	10853	2.26	6.0E-61	BE409310.1	EST_HUMAN	601300938F_NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1301	6299	11345	12.89	6.0E-61	AF119860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1609	6605	11688	2.82	6.0E-61	AA596303.1	EST_HUMAN	mm66h09.st_NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'
2068	7050	12158	0.95	6.0E-61	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
3234	8249	13270	13.87	6.0E-61	AU130889.1	EST_HUMAN	AU130689.NT2RP3_Homo sapiens cDNA clone NT2RP3001263 6'
359	5408	10420	0.88	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1639	6636	11706	3.51	5.0E-61	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
2865	7983	12987	2.15	5.0E-61	AL165279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3125	8141	13162	1.7	5.0E-61	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP) mRNA
3874	8875		1.68	5.0E-61	AJ228041.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21(q22; segment 1/3
4843	6408	10420	1.18	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
495	5531	10539	1.33	2.0E-61	3822829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1183	6194	11231	3.21	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-050400-147-d01 HT0513 Homo sapiens cDNA
1193	6194	11232	3.21	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-050400-147-d01 HT0513 Homo sapiens cDNA
1626	6623	11692	1.75	2.0E-61	NI53039.1	EST_HUMAN	W53d11.s1 Stares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248453 3' similar to gb:L25444 60S RIBOSOMAL PROTEIN L35A (HUMAN).
2570	7533		1.36	2.0E-61	NI39397.1	EST_HUMAN	W03f11.11 Stares melanocyte 2NbFM Homo sapiens cDNA clone IMAGE:270189 5'
432	5470		0.75	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
784	5785	10814	1.16	1.0E-61	5453829	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA
1732	6727		0.98	1.0E-61	U32657.1	NT	Human polymorphic trinucleotide repeat in X-linked retinitis pigmentosa (RP3) gene region
1821	6811	11804	4.18	1.0E-61	6005693	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2134	7114	12227	1.82	1.0E-61	AW6227281.1	EST_HUMAN	Wn11b09.y1 NCI_CGAP_L15_Homo sapiens cDNA clone IMAGE:2683369 5' similar to contains element
2781	7782	12807	2.42	1.0E-61	BE3863363.1	EST_HUMAN	MSR1 repetitive element;
3291	8302	13328	0.73	1.0E-61	7662319	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
4317	9309	14284	0.75	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK), mRNA
4317	9309	14285	0.75	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK), mRNA
4708	9683	14678	9.13	1.0E-61	AW288181.1	EST_HUMAN	U1-H-BW0-qt-b-08-0-U1.s1_NCI_CGAP_Sub Homo sapiens cDNA clone IMAGE:2732871 3'
4708	9683	14677	9.13	1.0E-61	AW288181.1	EST_HUMAN	U1-H-BW0-qt-b-08-0-U1.s1_NCI_CGAP_Sub Homo sapiens cDNA clone IMAGE:2732871 3'
4420	9410	14398	0.92	8.0E-62	AA850420.1	EST_HUMAN	W66h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone SW.POL_MLVRK_P31785 POL POLYPROTEIN;

Page 118 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1050	6097	11128	1.09	7.0E-62	AV714334	EST_HUMAN	AV714334 DCB Homo sapiens cDNA clone DCEAMA08 5'
3427	8435	13461	0.93	7.0E-62	P17480	SWISSPROT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIBODY NOR-90)
2930	7949		1.56	6.0E-62	U09410.1	NT	Human Zinc finger protein ZNF131 mRNA, partial cds
3300	8311		4.7	8.0E-62	11419255	NT	Homo sapiens CGI-58 protein (CGI-58) mRNA
413	5450	10470	3.65	5.0E-62	A1850528.1	EST_HUMAN	wu51a07.x1 NCI CGAP Lu38 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:G95_HUMAN
2341	7315	12435	3.43	5.0E-62	AJ271755.1	NT	Q05378 GOLGIN-96, contains element MER22, repetitive element;
2341	7316	12436	3.43	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
2515	7483	12599	0.98	5.0E-62	U39487.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
2515	7483	12600	0.88	5.0E-62	U39487.1	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
3334	8344	13382	2.46	5.0E-62	4506758	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
4201	9194	14176	1.82	5.0E-62	AA431093.1	EST_HUMAN	2w78ed9.s1 Soares,testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT
4427	9417		1.12	5.0E-62	AW805897.1	EST_HUMAN	RC5_NN1089-100500-021-1-03 NN1089 Homo sapiens cDNA
830	5850	10887	5.18	4.0E-62	AV161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
830	5850	10888	5.18	4.0E-62	AV161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
831	5850	10887	3.63	4.0E-62	AV161478.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
831	5850	10888	3.63	4.0E-62	AV161478.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2389	7360	12482	4.43	4.0E-62	A1827900.1	EST_HUMAN	wf12608.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
2389	7360	12483	4.43	4.0E-62	A1827900.1	EST_HUMAN	wf12608.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
3315	8326		7.88	4.0E-62	4557887	NT	gb:X57138_m1 HISTONE H2B.2 (HUMAN);
5023	8894	14887	0.97	4.0E-62	4758323	NT	Homo sapiens enhancer of zeste (Drosophila) homolog 2 (EZH2) mRNA
73	5151	10160	1.48	3.0E-62	4557784	NT	Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2) mRNA
2872	7980	13003	0.71	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
2872	7980	13004	0.71	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3615	8622	13630	8.12	3.0E-62	X52853.1	NT	Human cyclophilin-related processed pseudogene
1211	6211	11251	2.89	2.0E-62	AL163284.2	NT	Homo sapiens chitotriosidase 21 segment HS21C084

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1027	6037	11069	1.58	1.0E-62	AF246540.1	NT	Homo sapiens Intersecin 2 (SH3D1B) mRNA, complete cds
1512	6510	11597	15.3	1.0E-62	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
1763	6755	11840	1.92	1.0E-62	AA626207.1	EST_HUMAN	at70e11_r1 Scores_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1 CE03453
2844	7884	12882	1.18	1.0E-62	AL03944.1	EST_HUMAN	DKFZp566F104_r1 568 (synonym: hif2d2) Homo sapiens cDNA clone DKFZp566F104 5'
3339	8348		2.49	1.0E-62	AB040911.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
4395	9386	14369	1.63	1.0E-62	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
4956	9833	14911	0.98	1.0E-62	AA148822.1	EST_HUMAN	Z00b08_r1 Scores_pregnant uterus NBHU Homo sapiens cDNA clone IMAGE:491511 5' similar to SW:C581_BOVIN_P10897 CYTOCHROME B561.
336	5388	10395	1.82	9.0E-63	AW816405.1	EST_HUMAN	QV4-ST0234-181189-037-05 ST0234 Homo sapiens cDNA C18159 Human placenta cDNA (TFJulware) Homo sapiens cDNA clone GEN:558C10 5'
2284	7260		1.09	9.0E-63	C18159.1	EST_HUMAN	Homo sapiens mRNA for KIAA0350 protein, partial cds
3928	8928	13918	9.26	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
3928	8928	13919	9.28	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
5056	10026	14895	4.71	9.0E-63	AA015838.1	EST_HUMAN	z331d08_r1 Scores_reline N2p4HR Homo sapiens cDNA clone IMAGE:360591 5' similar to SW:UN13_CAEEL_P27715 PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13. [1];
2282	7258	12378	2.39	8.0E-63		4557734	NT
2313	7288	12409	5.14	8.0E-63	5031810	NT	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
3379	8387	13408	4.89	8.0E-63	AF198349.1	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3379	8387	13409	4.89	8.0E-63	AF198349.1	NT	Galus gallus Dach2 protein (Dach2), mRNA, complete cds
4143	9139	14122	3.27	8.0E-63	AL163208.2	NT	Galus gallus Dach2 protein (Dach2), mRNA, complete cds
916	5932		1.84	7.0E-63	AI872137.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C068 wnt5g11_x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2439608 3'
3247	8260	13282	0.7	4.0E-63	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3719	8723	13722	4.01	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
3719	8723	13723	2.01	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
1895	6883	11975	2.67	3.0E-63	AB018280.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2708	7863	12774	1.34	3.0E-63	J003101.1	NT	Human Mef-1 gene 1
2748	6219	11282	10.16	3.0E-63	6005963	NT	Homo sapiens zinc finger protein 144 (Met-18) (ZNF144), mRNA
191	5255	10267	2.47	2.0E-63	J07804.1	NT	Human DNA topoisomerase I mRNA, partial cds
198	5262	10275	1.85	2.0E-63	48855226	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
494	6530						Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GCLC) mRNA
816	6837	10872	4.72	2.0E-63	7857042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1533	6531	11591	1.52	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for RH blood CE group antigen polypeptide, complete cds

Page 120 of 209

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1633	6531	11592	1.62	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptides, complete cds
1729	6724	11802	3	2.0E-63	BE410739.1	EST_HUMAN	60130162/F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:36336103 5'
3083	8098	13114	1.58	2.0E-63	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-1), Alzheimer disease (APP), mRNA
3212	8227	13249	2.2	2.0E-63	AF108718.1	NT	Homo sapiens chromosome 3 subtelomeric region
3809	8812	13818	1.4	2.0E-63	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4716	9701	14687	1.23	2.0E-63	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4216	9209	14188	3.33	1.0E-63	FO8485.1	EST_HUMAN	HSCZVD111 normalized Infant brain cDNA Homo sapiens cDNA clone c-zvd11
4216	9209	14189	3.33	1.0E-63	FO8485.1	EST_HUMAN	HSCZVD111 normalized Infant brain cDNA Homo sapiens cDNA clone c-zvd11
1029	8039		9.14	8.0E-64	BE280798.1	EST_HUMAN	601155232/F1 NIH_MGC_24 Homo sapiens cDNA clone IMAGE:3139038 5'
3451	8459		0.9	7.0E-64	BS394321.1	EST_HUMAN	601311455/F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4593	9591	14570	3.25	7.0E-64	4507480	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
4593	9591	14571	3.25	7.0E-64	4507480	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
1684	6680	11753	5.45	6.0E-64	AI851892.1	EST_HUMAN	wb51e07_x1_NCI_CGAP_GCG Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1684	6680	11754	5.45	6.0E-64	AI851892.1	EST_HUMAN	wb51e07_x1_NCI_CGAP_GCG Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3049	8068	13074	5.09	6.0E-64	AW028446.1	EST_HUMAN	ww73603_x1_NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2528436 3'
3049	8068	13076	5.09	6.0E-64	AW028446.1	EST_HUMAN	ww73603_x1_NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2528436 3'
810	5831	10863	3.24	5.0E-64	AF231818.1	NT	Homo sapiens chromosome 21 unknown mRNA
810	5831	10864	3.24	5.0E-64	AF231819.1	NT	Homo sapiens chromosome 21 unknown mRNA
1318	6316	11384	2.38	5.0E-64	AB020701.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1397	6394	11448	1.35	5.0E-64	L40893.1	NT	Homo sapiens phosphoglucuronidase-related protein (PGM1RP) gene, complete cds
1397	6394	11449	1.35	5.0E-64	L40893.1	NT	Homo sapiens protein homolog mRNA, complete cds
1673	6669	11745	1.5	5.0E-64	U85358.1	NT	Homo sapiens KIAA0818 gene product (KIAA0818), mRNA
2753	6447	11608	4.17	5.0E-64	7662205	NT	Homo sapiens KIAA0818 gene product (KIAA0818), mRNA
2753	6447	11507	4.17	5.0E-64	7662205	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
3852	8854	13859	8.23	5.0E-64	AF017433.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
3988	8986	13972	1.02	5.0E-64	AB020701.1	NT	C18895 Human placenta cDNA (TFJuwara) Homo sapiens cDNA clone GEN-569E02 5'
2135	7115	12228	3.23	3.0E-64	C18895.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
3359	8367	13385	1.37	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
3359	8367	13386	1.37	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
1072	6080	11111	1.32	2.0E-64	AA609840.1	EST_HUMAN	af09d08_s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:1031151 3'

Page 121 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1374	6371	11420	5.42	2.0E-84	4157701	NT	Homo sapiens sif4E-like cap-binding protein 4(EHP) mRNA
2454	7424		1.92	2.0E-84	AI927030.1	EST_HUMAN	wo87b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element;
2459	7428	12544	2.92	2.0E-84	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2459	7428	12545	2.92	2.0E-84	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3067	8083	13097	0.81	2.0E-84	4504068	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
2563	53161	108256	1.58	1.0E-84	AF231919.1	NT	au60C01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to nucleic acid 9b121698 cds1 PROTHYROSIN ALPHA (HUMAN) contains element MSR1 repetitive element;
1741	6736	11812	61.83	1.0E-84	AI929419.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
2942	7861	12981	0.81	1.0E-84	4507334	NT	Homo sapiens synaptotagmin 1 (SYN1), mRNA
3432	8440	13487	5	1.0E-84	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α_2 β 2
3503	8511	13525	1.46	1.0E-84	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3503	8511	13526	1.46	1.0E-84	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3805	8808	13814	0.87	1.0E-84	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
2214	7191	12312	1.09	8.0E-85	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2214	7191	12313	1.09	8.0E-85	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
1039	6049	11079	3.17	8.0E-85	AV721898	HTB_Homo sapiens cDNA clone HTBBZC06 5'	
1880	6869		48.55	8.0E-85	AA556929.1	EST_HUMAN	nr88d10.51 NCI_CGAP_Pri11 Homo sapiens cDNA clone IMAGE:9899379 similar to gb:K03002 60S
625	5852	10856	0.86	5.0E-85	AF034604.1	NT	RIPOSOMAL PROTEIN L32 (HUMAN);
1335	6333	11381	1.94	5.0E-85	7661951	NT	Homo sapiens KIAA0158 protein mRNA, partial cds
1335	6333	11382	1.94	5.0E-85	7661951	NT	Homo sapiens KIAA0158 gene product (KIAA0158), mRNA
3181	8197	13220	1.88	5.0E-85	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3181	8197	13221	1.88	5.0E-85	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
193	9257	10270	3.82	4.0E-85	AL120479.1	EST_HUMAN	DKFZp761G108_r1761 (synonym: hany2) Homo sapiens cDNA clone DKFZp761G108 6'
736	5759	10781	1.07	4.0E-85	AI266468.1	EST_HUMAN	qmt46e01.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1891800 3'
736	5759	10782	1.07	4.0E-85	AI268468.1	EST_HUMAN	qmt46e01.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1891800 3'
1062	6070	11102	6.88	4.0E-85	4826735	NT	Homo sapiens fragile X mental retardation, autosomal transcript 1 (FXR1), mRNA
1455	6462	11511	18.84	4.0E-85	4508636	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA

Page 122 of 209

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2275	7261	12368	3.62	4.0E-65	BE221168.1	EST_HUMAN	hu25e01.x1 NCI_CGAP_Mar15 Homo sapiens cDNA clone IMAGE:3171102 3'
2275	7261	12369	3.52	4.0E-65	BE221169.1	EST_HUMAN	hu25e04.x1 NCI_CGAP_Mar15 Homo sapiens cDNA clone IMAGE:3171102 3'
3845	8847	13855	1.07	4.0E-65	AW893185.1	EST_HUMAN	RC2-BN0033-160200-013-a03 BN0033 Homo sapiens cDNA
96	5114	10185	1.82	3.0E-65	5031976.NT		Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
97	5114	10186	1.75	3.0E-65	5031976.NT		Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1212	7699	12112	3.12	3.0E-65	X78921.1	NT	H. sapiens HZF9 mRNA for zinc finger protein
1527	6524	11681	1.65	3.0E-65	4504628.NT		Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1787	8779	11871	1.62	3.0E-65	A1000652.1	EST_HUMAN	ov23103.s1 Seares testis_NIH Homo sapiens cDNA clone IMAGE:1658173 3' similar to contains element
2821	7940	12958	0.89	3.0E-65	4504628.NT	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
3203	8218	13241	0.83	3.0E-65	4504628.NT	NT	Homo sapiens mRNA for laminin, beta 1 (LAMB1) mRNA
3638	8644	13650	1.17	3.0E-65	A1000652.1	EST_HUMAN	ov23103.s1 Seares testis_NIH Homo sapiens cDNA clone IMAGE:1658173 3' similar to contains element
4515	9505	14485	1.45	3.0E-65	6912385.NT	MSR1 repetitive element;	
3320	8530	13351	6.2	2.0E-65	BF680294.1	EST_HUMAN	Homo sapiens rab GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
89	5166		1.12	1.0E-65	BF125544.1	EST_HUMAN	602155062F1 NIH MGC_851 Homo sapiens cDNA clone IMAGE:3285868 6'
534	6569	10572	1.79	1.0E-65	7657495.NT		601763488F1 NIH MGC_20 Homo sapiens cDNA clone IMAGE:4026601 6'
1889	6874	12079	1.12	1.0E-65	AB040946.1	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
3290	8301	13227	0.79	1.0E-65	BE466881.1	EST_HUMAN	Homo sapiens mRNA for KIAA1613 protein, partial cds
3892	8892	13890	1.89	1.0E-65	4504082.NT	NT	h224a09.x1 NCI_CGAP_GCB Homo sapiens cDNA clone IMAGE:3208888 3'
3892	8892	13891	1.89	1.0E-65	4504082.NT	NT	Homo sapiens glypican 4 (GPC4) mRNA
4084	9078	14068	3.43	1.0E-65	AW028340.1	EST_HUMAN	lw09c09.x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2643162 3'
4084	9078	14067	3.43	1.0E-65	AW028340.1	EST_HUMAN	lw09c09.x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2643152 3'
70	5149	10166	1.28	9.0E-66	AL160311.1	NT	Novel human gene mapping to chromosome 22
70	5149	10157	1.28	9.0E-66	AL160311.1	NT	Novel human gene mapping to chromosome 22
1336	6334	11383	2.47	9.0E-66	6031980.NT		Homo sapiens 28S proteasome-associated pd1 homolog (POH1) mRNA
1336	6334	11384	2.47	9.0E-66	5031980.NT		Homo sapiens 28S proteasome-associated pd1 homolog (POH1) mRNA
1453	6450		3.8	9.0E-66	M87299.1	NT	Human transposon-like element, partial
4553	8541	14526	0.86	9.0E-66	AL137163.1	NT	Novel human gene mapping to chromosome X
4240	9234	14216	1.02	6.0E-66	A1924653.1	EST_HUMAN	wn57n07.x1 NCI_CGAP_Lut9 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F16G8.4A
4240	9234	14217	1.02	6.0E-66	A1924653.1	EST_HUMAN	CE-85955;
							wn57n07.x1 NCI_CGAP_Lut9 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F16G9.4A

Page 123 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4240	9234	14218	1.02	8.0E-68	AI924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lui9 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15638.4A
1349	6346	11397	1.86	5.0E-68	BE084410.1	EST_HUMAN	CE:18595; RC4-BT0311-141188-011-005 BT0311 Homo sapiens cDNA
4939	9916	14695	0.81	5.0E-68	BE898644.1	EST_HUMAN	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951781 5'
4939	8916	14696	0.81	5.0E-68	BE898644.1	EST_HUMAN	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951781 5'
782	5503	10833	2.44	4.0E-68	6679816.16	NT	Mus musculus <i>regl</i> X mental retardation syndrome 1 homolog (Fmr1) mRNA
1688	6693	11769	1.24	4.0E-68	AW897768.1	EST_HUMAN	RC1-NN0083-100500-022-a02 NN0063 Homo sapiens cDNA
2217	7194	12316	2.12	4.0E-68	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2403	7374		2.81	4.0E-68	AI223364.1	NT	Homo sapiens gcm-line DNA upstream of <i>Ikappa</i> locus
4638	9823		4.38	4.0E-68	9835487.16	NT	Human endogenous retrovirus, complete genome
1402	6399	11455	34.87	3.0E-66	4502098.16	NT	Homo sapiens solute carrier family 2b (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1402	6399	11456	34.87	3.0E-66	4502098.16	NT	Homo sapiens solute carrier family 2b (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1936	6922	12020	1.02	3.0E-66	NT	Y27g12.1r1 Scares, multiple, sclerosis, 2Nb1HMSP Homo sapiens cDNA clone IMAGE:284328 5' similar to SW:H2B1_TIGCA_P35068_HISTONE_H2B_1/H2B_2. [2] PIR:B56612;	
1936	6922	12021	1.02	3.0E-66	NT	Y27g12.1r1 Scares, multiple, sclerosis, 2Nb1HMSP Homo sapiens cDNA clone IMAGE:284328 5' similar to SW:H2B1_TIGCA_P35068_HISTONE_H2B_1/H2B_2. [2] PIR:B56612;	
1936	6922	12022	1.02	3.0E-66	NT	Y27g12.1r1 Scares, multiple, sclerosis, 2Nb1HMSP Homo sapiens cDNA clone IMAGE:284328 5' similar to SW:H2B1_TIGCA_P35068_HISTONE_H2B_1/H2B_2. [2] PIR:B56612;	
2835	7695	12708	2.42	3.0E-66	11141880.16	NT	Homo sapiens TGf/beta-induced transcription factor 2 (TGf2), mRNA
3043	8050	130589	7.45	3.0E-66	7662223.16	NT	Homo sapiens KIAA0848 gene product (KIAA0848), mRNA
52	5133	10128	1.38	2.0E-66	7657334.16	NT	Homo sapiens Misshapen/Nlk-related kinase (Mlnk) mRNA
52	5133	10129	1.38	2.0E-66	7657334.16	NT	Homo sapiens Misshapen/Nlk-related kinase (Mlnk) mRNA
419	5077	10061	1.14	2.0E-66	4505524.16	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
419	5077	10062	1.14	2.0E-66	4505524.16	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
1791	6782	11874	2.62	2.0E-66	AL163301.2	NT	Homo sapiens chromosome 21 segment 1 (S21C101
2805	7924	12843	0.98	2.0E-66	X63859.1	NT	H. sapiens pseudogene for the low affinity IL-3 receptor
3679	8684	13686	0.82	2.0E-66	AL117233.1	NT	Novel human gene mapping to chromosome 1
4137	9132	14115	0.91	2.0E-66	8923768.16	NT	Homo sapiens histone deacetylase 8 (HDAC8 gene) (HS227724), mRNA
4521	9511	14495	39.41	2.0E-66	AJ33287.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
4521	9511	14496	39.41	2.0E-66	AJ33287.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B

Page 124 of 209
Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1644	6840			1.17	1.0E-86	BE881173.1	EST_HUMAN 6015083176F1 NIH MGC_71 Homo sapiens cDNA clone IMAGE:3908931 5'
2823	7844	12863		1.49	1.0E-86	AV717817.1	EST_HUMAN AV717817 DCB Homo sapiens cDNA clone DCBADC07 6'
2823	7844	12864		1.49	1.0E-86	AV717817.1	EST_HUMAN AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4260	7844	12863		3.88	1.0E-86	AV717817.1	EST_HUMAN AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4260	7844	12864		3.88	1.0E-86	AV717817.1	EST_HUMAN AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
379	5454	10471		4.95	7.0E-87	AW162232.1	EST_HUMAN EST96812 Testis Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid ZK533 au76d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104
1363	6360	11410		2.15	7.0E-87	AA386416.1	EST_HUMAN 2b56b05.r1 Soares, fetal liver, spleen_NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1523	6520	11576		1.98	7.0E-87	W85947.1	EST_HUMAN 2b56b05.r1 Soares, fetal liver, spleen_NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1523	6520	11677		1.88	7.0E-87	W85947.1	EST_HUMAN 2b56b05.r1 Soares, fetal liver, spleen_NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1982	6987	12072		1.31	7.0E-87	7657243	NT Homo sapiens Inositol 1,3,4-triphosphate 5' kinase (ITPK1), mRNA
1982	6987	12073		1.31	7.0E-87	7657243	NT Homo sapiens Inositol 1,3,4-triphosphate 5' kinase (ITPK1), mRNA
2738	5454	10471		4.77	7.0E-87	AW162232.1	EST_HUMAN au76d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104
556	5569	10590		1.53	8.0E-87	X689688.1	NT H. sapiens mRNA for acetyl-CoA carboxylase
787	5808	10538		2.36	8.0E-87	Z17227.1	NT Homo sapiens mRNA for transmembrane receptor protein
1254	6252	11283		1.35	8.0E-87	Y14320.1	NT Homo sapiens Plif96 gene, exons 3,4,5,6, & 7
3085	8111	13128		1.52	8.0E-87	4508424	NT Homo sapiens Relinablastone 1 (including osteosarcoma) (RB1) mRNA
3353	8361	13377		1.44	8.0E-87	4507332	NT Homo sapiens Synapsin III (SYN3) mRNA, and translated products
3353	8361	13378		1.44	8.0E-87	4507332	NT Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4567	9555	14512		3.45	8.0E-87	7657020	NT Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4567	9555	14513		3.45	8.0E-87	7657020	NT Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4805	9789			0.88	8.0E-87	4507848	NT Homo sapiens Ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
5012	9883	14958		1.01	8.0E-87	AF016898.1	NT Homo sapiens B-ATF gene, complete cds
5012	9883	14959		1.01	8.0E-87	AF016899.1	NT Homo sapiens B-ATF gene, complete cds
3150	8166	13186		2.02	5.0E-87	AF009860.1	NT Homo sapiens T cell receptor beta locus, TCRBV1232 region
1308	6306	11356		1.2	4.0E-87	R90819.1	EST_HUMAN ym02d11.11 Soares adult brain N2b4-H5FY Homo sapiens cDNA clone IMAGE:167263 5'
2741	5654	10659		1.65	3.0E-87	AA33768.1	EST_HUMAN EST37603 Embryo, 8 week Homo sapiens cDNA 5' end
3371	8379	13399		1.01	3.0E-87	BE054410.1	EST_HUMAN RC4-BT0311-141188-011-016 BT0311 Homo sapiens cDNA
4555	9543	14528		3.04	3.0E-87	AW869159.1	EST_HUMAN MR3-SN00868-040500-008-01 SN0068 Homo sapiens cDNA
188	5252	10263		1.1	2.0E-87	BE348364.1	EST_HUMAN lw16g09.x1 NCI CGAP_L124 Homo sapiens cDNA clone IMAGE:3183138 3' similar to WP:F23H11.9
835	5854	10894		5.38	2.0E-87	AW818405.1	EST_HUMAN Cf09817; Q174-ST0234-181199-037-705 ST0234 Homo sapiens cDNA

Page 125 of 209
Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1088 6095			2.11	2.0E-67	AF167460.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4 ba72905.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:094892 094892
1815 6834	11924		1.28	2.0E-67	BE303037.1	EST_HUMAN	KIAA0798 PROTEIN; ba72905.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:094892 094892
1845 6834	11925		1.28	2.0E-67	BE303037.1	EST_HUMAN	KIAA0798 PROTEIN; ba72905.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:094892 094892
2178 7158	122777		1.81	2.0E-67	114229461	NT	Homo sapiens hypothetical protein dJ462023.2 (D)J462023.2, mRNA ba72905.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:094892 094892
2179 7158	12278		1.81	2.0E-67	114229461	NT	Homo sapiens hypothetical protein dJ462023.2 (D)J462023.2, mRNA ba72905.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:094892 094892
2323 7297	12419		1.29	2.0E-67	AF308561.1	NT	Homo sapiens KRAB zinc finger protein ZFQR mRNA, complete cds ba72905.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:094892 094892
2364 7338	124655		2.28	2.0E-67	4758795	NT	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA ba72905.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:094892 094892
3387 8395	13419		3.68	2.0E-67	AA025755.1	EST_HUMAN	zub91901.61 Soares, Testes_NIH Homo sapiens cDNA clone IMAGE:745392 3' ba72905.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:745392 3'
3896 8896	13894		2.87	2.0E-67	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100 ba72905.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:745392 3'
251 5311	10322		2.94	1.0E-67	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA ba72905.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:745392 3'
698 5722	10738		2.16	1.0E-67	AA702794.1	EST_HUMAN	z80b04.s1 Soares, fetal liver, spleen, 1NF1_S_1 Homo sapiens cDNA clone IMAGE:3852254 5' ba72905.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3852254 5'
2411 7091	12206		2.23	8.0E-68	BE870732.1	EST_HUMAN	601448558F NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5' ba72905.y1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5'
3778 8781	13784		4.83	8.0E-68	AA209456.1	EST_HUMAN	SW-SAV_SULAC Q07590 SAV PROTEIN; ba72905.y1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5' similar to zq82h10.1r1 Strategene INT neuron (#937233) Homo sapiens cDNA clone IMAGE:3852254 5'
3778 8781	13785		4.83	8.0E-68	AA209456.1	EST_HUMAN	SW-SAV_SULAC Q07590 SAV PROTEIN; ba72905.y1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5'
1851 6840			1.83	8.0E-68	AW503842.1	EST_HUMAN	U1-HFBN0-rib-c-07-07-01 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078924 5' ba72905.y1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078924 5'
809 5830	10861		3.82	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA ba72905.y1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078924 5'
809 5830	10862		3.82	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA ba72905.y1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078924 5'
2707 7684	12775		1.09	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA ba72905.y1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078924 5'
3074 8090	13104		3.02	5.0E-68	AB037052.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds ba72905.y1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078924 5'
4057 8051			0.68	5.0E-68	4826967	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA ba72905.y1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078924 5'
4363 9354	14333		0.66	5.0E-68	AL157645.1	EST_HUMAN	DKFZp547D207_r1 547 (synonym: fib1) Homo sapiens cDNA clone DKFZp547D207 5' ba72905.y1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078924 5'
2456 7426	12540		1.15	4.0E-68	11421368	NT	Homo sapiens transcription factor NRF (NRF), mRNA ba72905.y1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078924 5'
2458 7426	12541		1.15	4.0E-68	11421368	NT	Homo sapiens transcription factor NRF (NRF), mRNA ba72905.y1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078924 5'
4816 9800			16.14	4.0E-68	PO4406	SVISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER Mus musculus G-protein coupled receptor GPR73 (Gp73) mRNA, complete cds ba72905.y1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078924 5'
3577 8584	135689		7.2	3.0E-68	AF236682.1	NT	Cricetulus longicaudatus mRNA for EF-1 alpha, complete cds ba72905.y1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078924 5'
2791 10054			39.36	2.0E-68	D00522.1	NT	Tfl15022.x1 NCI CGAP_C1L1 Homo sapiens cDNA clone IMAGE:3200747 3' similar to TR:080828 080828
3915 8915	13909		0.68	2.0E-68	BE075768.1	EST_HUMAN	HYPOTHETICAL 88.8 KD PROTEIN; ba72905.y1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3200747 3'
4543 9532	14520		1.84	2.0E-68	AB008681.1	NT	Homo sapiens gene for activin receptor type IIb, complete cds ba72905.y1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3200747 3'

Page 126 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
78	5155	10166	0.94	1.0E-68	4505222	NT	Hom sapiens meningioma disrupted in balanced translocation 1 (MNN1) mRNA
284	5351	10384	11.12	1.0E-69	AAW16405.1	EST_HUMAN	QV4-S-T0234-181188-037-705 S70234 Homo sapiens cDNA
2180	7169	12289	1.74	1.0E-68	AB011149.1	NT	Hom sapiens mRNA for KIAA0577 protein, complete cds
2180	7169	12290	1.74	1.0E-68	AB011149.1	NT	Hom sapiens mRNA for KIAA0577 protein, complete cds
3803	8903	13801	0.97	1.0E-68	BE286032.1	EST_HUMAN	601177002F NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5
4801	9880	14849	1.18	1.0E-68	BE286032.1	EST_HUMAN	601177002F NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5
20	5100	10083	7.87	8.0E-69	5031976	NT	Hom sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
20	5100	10084	7.87	8.0E-69	5031976	NT	Hom sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1011	6021	11050	2.59	8.0E-69	5031980	NT	Hom sapiens 26S proteasome-associated pab1 homolog (POH1) mRNA
1011	6021	11051	2.59	8.0E-69	5031980	NT	Hom sapiens 26S proteasome-associated pab1 homolog (POH1) mRNA
5035	10008	14977	0.94	8.0E-69	4507164	NT	Hom sapiens nuclear antigen Sp100 (SP100) mRNA
3302	8313		1.28	8.0E-69	AJ237744.1	NT	Hom sapiens RIBIR gene (partial), exon 12
516	6551		0.99	4.0E-69	AB73630.1	EST_HUMAN	wm2611.x1 NC1 CGAP_U14 Homo sapiens cDNA clone IMAGE:2437125 3
385	6460	10478	5.07	3.0E-69	BE258012.1	EST_HUMAN	601110371F NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5'
609	6325	10336	2.03	3.0E-69	AF221712.1	NT	Hom sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
							yd08a02.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:24880 5' similar to SP-A48836
4804	9788	14771	1.63	3.0E-69	T80514.1	EST_HUMAN	A48838 SPEGF III-EGF REPEAT-CONTAINING FIBRONECTIN-LIKE PROTEIN - SEA URCHIN;
4971	8865	13854	0.97	3.0E-69	AB037732.1	NT	Hom sapiens mRNA for KIAA1311 protein, partial cds
129	5438	10457	1.68	3.0E-69	AI765888.1	EST_HUMAN	wn86g08.x1 NC1 CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385758 3'
129	5438	10458	2.01	2.0E-69	AF160252.1	NT	Hom sapiens KIAA0553 protein gene, complete cds; and alpha/beta protein gene, partial cds
402	5438	10457	2.01	2.0E-69	AF160252.1	NT	Hom sapiens KIAA0553 protein gene, complete cds; and alpha/beta protein gene, partial cds
402	5438	10458	6.22	2.0E-69	AF160252.1	NT	Hom sapiens KIAA0553 protein gene, complete cds; and alpha/beta protein gene, partial cds
1846	68335	11926	5.22	2.0E-69	AF160252.1	NT	Hom sapiens KIAA0553 protein gene, complete cds; and alpha/beta protein gene, partial cds
2770	7791		2.69	2.0E-69	BE257857.1	EST_HUMAN	601103944F NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350074 5'
4970	9947	14924	3.44	2.0E-69	AA431157.1	EST_HUMAN	2N71902.r1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:781682 5'
4970	9947	14925	1.2	2.0E-69	4504148	NT	Hom sapiens glutamate receptor, metabotropic B (GRMB) mRNA
1684	6860	11734	1.2	2.0E-69	4504148	NT	Hom sapiens glutamate receptor, metabotropic B (GRMB) mRNA
2270	7768	12363	1.7	1.0E-69	AF053798.1	NT	Rattus norvegicus brain specific contactin-binding protein CBP80 mRNA, partial cds
4248	9242	14226	1.55	8.0E-70	AA230303.1	EST_HUMAN	ne13412.r1 NC1 CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1008023
1777	6769	11860	2	8.0E-70	L77568.1	NT	Hom sapiens DGS-1 mRNA, 3' end
1777	6769	11861	4.69	7.0E-70	AI497807.1	EST_HUMAN	lm8801.x1 NC1 CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163305 3'
1880	6879	11969	4.59	7.0E-70	AI497807.1	EST_HUMAN	lm8901.x1 NC1 CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163305 3'
			2.37	7.0E-70	AA292955.1	EST_HUMAN	2N15h04.r1 NC1 CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713239 5'

Table 4
Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2011	6984		6.81	7.0E-70	5031688	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA
4103	9097	14083	3.65	7.0E-70	4757723	NT	Homo sapiens adenylyl cyclase 3 (ADCY3) mRNA
860	5878	10820	4.09	6.0E-70	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-1; Alzheimer disease) (APP), mRNA
2078	7059	12169	4.32	6.0E-70	M30898.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2437	7408	12825	1.12	6.0E-70	8923899	NT	Homo sapiens CMIP-N-acetylneuraminc acid synthase (LOC559907), mRNA
2481	7772	12861	1.63	6.0E-70	7682307	NT	Homo sapiens KIAA0782 gene product (KIAA0782), mRNA
2481	7772	12862	1.63	6.0E-70	7662307	NT	Homo sapiens KIAA0782 gene product (KIAA0782), mRNA
1554	6851	11810	3.24	3.0E-70	BE071798.1	EST_HUMAN	RC0-BT0522-071289-011-1a12_BT0522_Homo sapiens cDNA
1554	6851	11811	3.24	3.0E-70	BE071798.1	EST_HUMAN	RC0-BT0522-071289-011-1a12_BT0522_Homo sapiens cDNA
39	5119	10107	1.16	2.0E-70	AF012872.1	NT	Homosapiens phosphatidylinositol 4-kinase 230 (PLAK230) mRNA, complete cds
680	5706	10714	11.75	2.0E-70	N42161.1	EST_HUMAN	Y07810_r1 Soares melanocyte 2NbFM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3H1_RAT_P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
680	5705	10716	11.75	2.0E-70	N42161.1	EST_HUMAN	Y07810_r1 Soares melanocyte 2NbFM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3H1_RAT_P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
685	5719	10737	1.73	2.0E-70	AI246898.1	EST_HUMAN	Q51101_x1_NCL_CGAP_Fan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1005	6015	11045	2.33	2.0E-70	8923669	NT	Homosapiens hypothetical protein FLJ20758 (FLJ20758) mRNA
1165	6168	11202	1.5	2.0E-70	7661983	NT	Homo sapiens KIAA0183 gene product (KIAA0183), mRNA
1165	6168	11203	1.5	2.0E-70	7661983	NT	Homo sapiens KIAA0183 gene product (KIAA0183), mRNA
1615	6612	11678	1.22	2.0E-70	AA180093.1	EST_HUMAN	ZP4505_r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:612441 5' similar to TR:G1041283 G1041283 D2085.5 ;
1615	6612	11879	1.22	2.0E-70	AA180093.1	EST_HUMAN	ZP4505_r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:612441 5' similar to TR:G1041283 G1041283 D2085.5 ;
1703	6698	11774	1.85	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C3022
2256	7233		7.98	2.0E-70	AA054010.1	EST_HUMAN	ZP4804_r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A
2416	7388	12506	1.57	2.0E-70	AB01173.1	NT	Homo sapiens mRNA for KIAA0861 protein, partial cds
3728	8732	13730	1.26	2.0E-70	AL133207.2	NT	Novel human gene mapping to chromosome X
3838	8840	13847	1.17	2.0E-70	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
3838	8935	13928	4.94	2.0E-70	M69181.1	NT	Human muscle myosin heavy chain-B (MYH10) mRNA, partial cds
4068	9063	14051	1.03	2.0E-70	L78810.1	NT	Homosapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4068	9063	14052	1.03	2.0E-70	L78810.1	NT	Homosapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
3309	8320		3.18	1.0E-70	4507476	NT	Homosapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA

Page 128 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2148	7127	12244	14.02	5.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4001	8897	13886	0.87	5.0E-71	AW816405.1	EST_HUMAN	CV4-S10234-181198-037-705 S10234_Homo sapiens cDNA
103	5180	10191	0.97	4.0E-71	4507592	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
348	5400	10409	216.31	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
348	5400	10410	215.31	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2816	7838	12851	1.81	4.0E-71	4605880	NT	Homo sapiens plastinogen (PLG) mRNA
4504	9298	14282	7.98	4.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4927	9811	14782	6.12	4.0E-71	7657602	NT	Homo sapiens putative home-binding protein (SOUL) mRNA
1210	6210	11250	16.81	2.0E-71	AL163206.2	NT	Homo sapiens chromosome 21 segment 1521C006
632	6660	10685	1.87	1.0E-71	AI077827.1	EST_HUMAN	cy15603.51_Seques_senescent_fibroblasts_NbHSF_Homo sapiens cDNA clone IMAGE:16865916 3' similar to contains LOR,b2 LOR1 repetitive element;
827	5944	10978	6.13	1.0E-71	77059281	NT	Homo sapiens neuronal cell death-related protein (LOC51616) mRNA
1083	6090	11119	4.33	1.0E-71	AF205890.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
1320	63118	11368	8.38	1.0E-71	AF012872.1	NT	Homo sapiens phosphotyrosine 4-kinase 230 (p4K230) mRNA, complete cds
2029	7012	12120	1.35	1.0E-71	AB017071.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2028	7012	12121	1.35	1.0E-71	AB017071.1	NT	Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEY1), mRNA
2621	7883	12693	3.09	1.0E-71	7657153	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3422	8450	13456	2.38	1.0E-71	AF119865.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3516	8524	13534	6.34	1.0E-71	AF246218.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3516	8524	13535	6.34	1.0E-71	AF246218.1	NT	02_16_Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA
3563	8570	13575	0.73	1.0E-71	BE122850.1	EST_HUMAN	clone 02_15 5' similar to Homo sapiens chromosome 19
3583	8570	13576	0.73	1.0E-71	BE122850.1	EST_HUMAN	clone 02_15 5' similar to Homo sapiens chromosome 19
3858	8662	13867	1.73	1.0E-71	AF218904.1	NT	Homo sapiens altracin precursor (ATRN) gene, exon 19
4345	9336	14319	2.05	1.0E-71	D28478.1	NT	Human mRNA for KIAA0045 gene, complete cds
4460	9450	14431	1.19	1.0E-71	H23176.1	EST_HUMAN	ym58h10.11_Seques_infant brain 1N1B_Homo sapiens cDNA clone IMAGE:526283 5'
405	5441	10460	0.74	9.0E-72	AI857635.1	EST_HUMAN	wk95p03.x1_NCL_CGAP_L119_Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:086705 086705
405	5441	10461	0.74	9.0E-72	AI857635.1	EST_HUMAN	wk95p03.x1_NCL_CGAP_L119_Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:086706 086706
3988	8992	13977	1.54	.70E-72	45018681	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA

Page 129 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3986	8992	13978	1.54	7.0E-72	4501866	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
3996	8992	13979	1.54	7.0E-72	4501866	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
64	5144	10148	2.81	BF333707.1	EST_HUMAN	Q90- <i>CS0010-150900-398-e11</i> CS0010_Homo sapiens cDNA	
64	5144	10149	2.81	5.0E-72	BF333707.1	EST_HUMAN	Q90- <i>CS0010-150900-398-e11</i> CS0010_Homo sapiens cDNA
65	5144	10148	18.08	5.0E-72	BF333707.1	EST_HUMAN	Q90- <i>CS0010-150900-398-e11</i> CS0010_Homo sapiens cDNA
65	5144	10149	18.08	5.0E-72	BF333707.1	EST_HUMAN	Q90- <i>CS0010-150900-398-e11</i> CS0010_Homo sapiens cDNA
1122	6128	2.73	6.0E-72	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds	
4676	9881		1.32	4.0E-72	11034844	NT	Homo sapiens hypothetical protein <i>dj1057B20.2</i> (Dj1057B20.2), mRNA
6048	10019	14888	1.07	4.0E-72	AB0331104.1	NT	Homo sapiens mRNA for <i>KIAA1278</i> protein, partial cds
19	5099	10082	2.48	3.0E-72	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBECF1), mRNA
892	5910		1.27	3.0E-72	AA723823.1	EST_HUMAN	eh63ad6.s1 Soares testis_NHT_Homo sapiens cDNA clone 1310280 3'
1137	6142	11171	11.37	3.0E-72	U16308.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1137	6142	11172	11.37	3.0E-72	U16308.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1174	6177	11211	1.12	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1174	6177	11212	1.12	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
3001	8018	13032	12.79	3.0E-72	AJ280643.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
3205	8220	13242	2.5	3.0E-72	8923548	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
3732	8738	13734	3.01	3.0E-72	S7758.1	NT	TCR V delta 2-C alpha = T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction)
4414	8404	14389	3.65	3.0E-72	11416188	NT	[Human, precursor B-cell line REH, mRNA Partial, 211 nt]
4621	9606	14589	1.08	3.0E-72	AF167572.1	NT	Hom sapiens protein methyltransferase (JBP1), mRNA, complete cds
4621	9606	14594	1.08	3.0E-72	AF167572.1	NT	Hom sapiens protein methyltransferase (JBP1), mRNA, complete cds
2022	7005	12110	1.03	1.0E-72	AA846225.1	EST_HUMAN	elB3d02.s1 Soares_ parathyroid tumor_NHHPA_Homo sapiens cDNA clone IMAGE:1387395 3'
1433	8430	11486	1.26	9.0E-73	AW374968.1	EST_HUMAN	MRO-C10063-07/1089-002-r11 C10063_Homo sapiens cDNA
1021	6030	11060	3.27	8.0E-73	AW071755.1	EST_HUMAN	ws65c08_x1_NCI_CGAP_Bm25_Homo sapiens cDNA clone IMAGE:2501098 3' similar to TR:Q588650
1117	6123	11153	0.98	7.0E-73	8923290	NT	Q59050_HYPOTHETICAL PROTEIN MJ1656 ;
3227	8242	13284	1.64	7.0E-73	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
4787	9771		1.48	7.0E-73	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
157	6223		1.71	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018

Page 130 of 209

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1321	6319	11367	1.38	3.0E-73	AW843798.1	EST_HUMAN	CM0-CN0044-2601-184-008 CN0044 Homo sapiens cDNA
1825	6815	11808	1.1	3.0E-73	11435913	NT	Homo sapiens Home-binding protein (HEBP), mRNA
1825	6815	11910	1.1	3.0E-73	11435913	NT	Homo sapiens Home-binding protein (HEBP), mRNA
841	58830	10800	2.37	2.0E-73	AF139897.1	NT	Homo sapiens BASS1 (BASS1) mRNA, partial cds
1906	68833		3.12	2.0E-73	AW8588081.1	EST_HUMAN	RC3-NN0068-270400-011->04 NN0068 Homo sapiens cDNA
3108	8124	13143	3.89	2.0E-73	4502552	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
4311	9303		1.02	2.0E-73	AL169283.2	NT	Homo sapiens chromosome 21 segment HS21C083
1745	6740	11819	2.61	1.0E-73	AL121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'
2413	7384	12503	1.04	1.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
731	6754	10776	1.78	8.0E-74	4557426	NT	Homo sapiens CD38-like 4 (CD38L4) mRNA
1909	6895	11889	2.57	7.0E-74	AJ001689.1	NT	Homo sapiens NK22D gene, exon 10
3253	8266	13288	1.22	7.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
							Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
1105	6112	11143	4	6.0E-74	AF109807.1	NT	
1587	6584	11845	0.92	6.0E-74	AW263177.1	EST_HUMAN	xn78g07-x1_Scarce_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700596 3'
2252	7229	12347	63.86	6.0E-74	BE388280.1	EST_HUMAN	601283521F1 NIH MGCG_44 Homo sapiens cDNA clone IMAGE:3605453 6'
2252	7229	12348	53.86	6.0E-74	BE388280.1	EST_HUMAN	601283521F1 NIH MGCG_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2793	7813	12831	0.97	6.0E-74	AW014099.1	EST_HUMAN	U1-H-Bio-aaH-h-03-0-U1_s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708385 3'
2793	7813	12832	0.97	6.0E-74	AW014099.1	EST_HUMAN	U1-H-Bio-aaH-h-03-0-U1_s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708385 3'
3631	8637	13642	1.37	6.0E-74	BE048846.1	EST_HUMAN	hr54611-x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
3631	8637	13643	1.37	6.0E-74	BE048846.1	EST_HUMAN	hr54611-x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
4866	9846	14821	1.55	6.0E-74	4758136	NT	Homo sapiens DEAD1H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
4866	9846	14822	1.55	6.0E-74	4758135	NT	Homo sapiens DEAD1H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
894	5912	10951	2.15	5.0E-74	AW020988.1	EST_HUMAN	df17c09_y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2630	7560		6.51	5.0E-74	AW362756.1	EST_HUMAN	PM0-CT0289-271088-001->07 CT0289 Homo sapiens cDNA
277	6335	10349	6.48	4.0E-74	DB7676.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
842	5881	10801	5.8	4.0E-74	AB0286942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
1922	6908	12002	1.42	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
1922	6908	12003	1.42	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
2019	7002	12106	6.12	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA

Page 131 of 209
Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar ('Top') Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2019	7002	12107	5.12	4.0E-74	4508192	NT	Homo sapiens proteasome (prosome, macropeptidase) subunit, beta type, 1 (PSMB1) mRNA
2074	7056	12166	1.18	4.0E-74	AB032984.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
3017	8034	13045	5.03	4.0E-74	AJ008976.1	NT	Homo sapiens PLP gene
3449	8457	13483	0.81	4.0E-74	AL183210.2	NT	Homo sapiens chitonotromin 21 segment HS21C010
3850	8948	13937	1.22	4.0E-74	AL183247.2	NT	Homo sapiens chitonotromin 21 segment HS21C047
4125	9415	14402	1.98	4.0E-74	7682183	NT	Homo sapiens KIAA0589 gene product (KIAA0589) mRNA
4481	9471	14452	1.19	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
4902	9881	14850	1.02	4.0E-74	4504326	NT	Homo sapiens hydroxacyl-Coenzyme A thiolesterase/3-ketoacyl-Coenzyme A thiolesterase/enoyl-Coenzyme A thiolesterase (trifunctional protein), beta subunit (HADHB) mRNA
4902	9881	14851	1.02	4.0E-74	4504326	NT	Homo sapiens hydroxacyl-Coenzyme A thiolesterase (trifunctional protein), beta subunit (HADHB) mRNA
5011	9982	14957	0.81	4.0E-74	AB037853.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
943	5960	10933	263.61	2.0E-74	7682491	NT	Homo sapiens glyceradehyde-3-phosphate dehydrogenase (GAPD) mRNA
943	5960	10994	263.61	2.0E-74	7682491	NT	Homo sapiens glyceradehyde-3-phosphate dehydrogenase (GAPD) mRNA
1156	6160	11184	1.2	2.0E-74	AF020592.1	NT	Human endogenous retrovirus HERV-K-T47D
1225	6224	11270	2.76	2.0E-74	AI950528.1	EST_HUMAN	W51607_X1 NCI CGAP_L128 Homo sapiens cDNA clone IMAGE:25472043 similar to SW:GG85_HUMAN Q08378 GOLGIN-85; contains element MER22 repetitive element;
1550	6557	11818	3.33	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
1550	6557	11619	3.33	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2526	7492	12812	3.89	2.0E-74	AI557280.1	EST_HUMAN	PT2.1_15_G11.1 tumor 2 Homo sapiens cDNA 3'
4848	6828	14802	2.77	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
4848	6828	14803	2.77	2.0E-74	AL355092.1	NT	Human plakophilin-related protein 1b mRNA, 3' end
4850	6832	14807	3.98	2.0E-74	J02863.1	NT	Homo sapiens Misshephen/NIK-related kinase (MINK) mRNA
64	5135	10132	2.92	1.0E-74	7657334	NT	Human plakophilin-related protein 1b mRNA, 3' end
335	5387	10394	4.23	1.0E-74	AW816405.1	EST_HUMAN	QV4-ST0234-181198-037-405 ST0234 Homo sapiens cDNA
495	6532	10539	1.19	1.0E-74	8922829	NT	Homo sapiens hypothetical protein FLJ11028 (FLJ11028) mRNA
503	6538	10544	28.75	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
596	6627	10526	2.38	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
984	5999	11030	2.04	1.0E-74	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C048
2165	7144	12262	5	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XN, complete cds
3066	8082	13086	3.19	1.0E-74	4758697	NT	Homo sapiens meprosidase, alpha, class 2A, member 1 (MAN2A1) mRNA
3822	8824	13831	0.61	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRK1) mRNA

Page 132 of 209

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3822	8924	13932	0.97	1.0E-74	4504416	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3861	8963	13988	4.97	1.0E-74	AL189268.2	NT	Homo sapiens chromosome 21 segment HS21C06B
4145	9140	14124	1.12	1.0E-74	BE187769.1	EST_HUMAN	h273h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213863 3' similar to WP:BO5111.12
2573	7536		3.52	8.0E-75	AF478228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
2257	7234	12352	0.98	6.0E-76	AI817416.1	EST_HUMAN	wk28a08.x1 NCI_CGAP_Pr722 Homo sapiens cDNA clone IMAGE:24117654 3' similar to gb:M14123_cds4
1112	6184	10163	3.57	4.0E-76	BE081333.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN (HUMAN); QV1-BT0592.21/0200-079-e02_BT0632 Homo sapiens cDNA
458	5493		0.99	4.0E-76	NS8757.1	EST_HUMAN	ye80h08.r1 Sarcos melanoctye 2NbHM Homo sapiens cDNA clone IMAGE:268065_6'
1728	6723	11801	1.27	4.0E-75	AW897230.1	EST_HUMAN	CM0-NN0057-150400-335-a11 NN0057 Homo sapiens cDNA
2776	7797	12818	5.17	4.0E-76	BE408464.1	EST_HUMAN	601303866F NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344_5'
3421	8429	13465	0.97	4.0E-75	8922687	NT	Homo sapiens hypothetical protein FLJ10747 (FLJ10747), mRNA
987	6002	11033	2.28	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
988	6002	11033	2.29	3.0E-75	AF167823.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1800	6791	11881	1.84	3.0E-75	AB011163.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
1887	6978	11986	2.26	3.0E-75	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
2053	7035	12147	0.92	3.0E-75	4507334	NT	Homo sapiens synaptotagmin 1 (SYN1), mRNA
2358	7330	12446	3.59	3.0E-75	7330.1	NT	Homo sapiens synaptosomal-associated protein, 28kD (SNAP29) mRNA
2955	7974	12989	0.9	3.0E-75	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3116	8132	13161	1.01	3.0E-75	AB011163.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3273	8225	13308	0.75	3.0E-75	MT2393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3273	8285	13309	0.75	3.0E-75	MT2393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4044	9040	14031	1.53	3.0E-75	DB7675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4314	9306	14280	0.82	3.0E-75	7682421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
4996	9868		0.82	3.0E-75	AL163209.2	NT	Hom sapiens chromosome 21 segment HS21C009
2239	7216	12334	30.85	1.0E-75	AW168135.1	EST_HUMAN	xg50dp2.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:26322707 3' similar to contains PTR7.11
2876	7895	12919	3.35	1.0E-75	X52221.1	NT	H.sapiens EFCC2 gene, exons 1 & 2 (partis)
4952	9540	14525	1.71	1.0E-75	BE278301.1	EST_HUMAN	601167633F NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272_5'
4983	9965	14943	1.23	1.0E-75	BE894182.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303_5'
45	5126	10116	3.62	9.0E-76	AI652648.1	EST_HUMAN	wb30b10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:075236_O75235
45	5126	10117	3.62	9.0E-76	AI652648.1	EST_HUMAN	wb30b10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:075235_O75235

Page 133 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
924	6941	10974	0.84	8.0E-76	4504374	NT	Homo sapiens. H factor 1 (complement) (Hf1) mRNA
924	6941	10975	0.84	8.0E-76	4504374	NT	Homo sapiens. H factor 1 (complement) (Hf1) mRNA
2839	7859	12879	1.17	8.0E-76	7706724	NT	Homo sapiens. mediator (Sur2) mRNA
787	57788	10817	1.86	7.0E-76	5016092	NT	Homo sapiens. dihydrodipamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3220	8235	13256	3.47	7.0E-76	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 5A (PDE8A) mRNA, partial cds
3226	8241	13263	7.12	7.0E-76	4505052	NT	Homo sapiens lymphocyte antigen 76 (LY76) mRNA, and translated products
4246	9240	14223	4.97	7.0E-76	4507184	NT	Homo sapiens. sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4246	9240	14224	4.97	7.0E-76	4507184	NT	Homo sapiens. sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1214	6213		16.84	6.0E-76	BE398263.1	EST_HUMAN	601312018F1_NIH_MGC_44_Homo sapiens cDNA clone IMAGE:3658757 6'
1803	6890	11983	15.24	5.0E-78	D63874.1	NT	Human mRNA for HMG-1, complete cds
1803	6890	11984	15.24	5.0E-78	D63874.1	NT	Human mRNA for HMG-1, complete cds
1803	6890	11985	15.24	5.0E-78	D63874.1	NT	Human mRNA for HMG-1, complete cds
3134	8150	13172	0.8	4.0E-76	BB1814098.1	EST_HUMAN	QV3-BN0047-270700-263-006 BN0047 Homo sapiens cDNA
623	10653		1.54	3.0E-76	BF518262.1	EST_HUMAN	UI-H-BW1-anz-b-04-0-U1_si_NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3033862 3'
623	5650	10654	1.54	3.0E-76	BF518262.1	EST_HUMAN	UI-H-BW1-anz-b-04-0-U1_si_NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3033862 3'
1584	6561	11623	21.41	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1584	6561	11624	21.41	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3344	8353	13370	6.25	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 S10300 Homo sapiens cDNA
3344	8353	13371	6.25	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 S10300 Homo sapiens cDNA
279	5337	10351	1	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRD11, complete cds
340	5392	10398	1.94	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRD11, complete cds
340	5392	10399	1.94	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRD11, complete cds
458	5495		1.42	2.0E-76	4557662	NT	Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA
585	5616	10616	1.68	2.0E-76	4503944	NT	Homo sapiens glucagon (GCG) mRNA
1014	6024	11056	1.18	2.0E-76	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1504	6502	11658	2.34	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1504	6502	11559	2.34	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
2768	7789	12811	3.35	2.0E-76	P23268	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F6
3223	8238	13260	1.89	2.0E-76	AA445892.1	EST_HUMAN	ZW64602_s1_Sores. testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:1TB5_HUMAN
3223	8238	13261	1.89	2.0E-76	AA445892.1	EST_HUMAN	P18034 INTEGRIN BETA-5 SUBUNIT PRECURSOR.; ZW64602_s1_Sores. testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:1TB5_HUMAN

Page 134 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3896	8404	13430	1.04	2.0E-76	AB21149.1	EST_HUMAN	ec83b02,56 Stratagene lung (#8372/10) Homo sapiens cDNA clone IMAGE:888183 5' similar to TR014591 O14591 SIMILARITY TO P22059;
3892	8686	13688	7.33	2.0E-76	AA40700.1	EST_HUMAN	zu70911-11 Soares testis_NH7 Homo sapiens cDNA clone IMAGE:743398 5' similar to WP:R05D3.2 CE00281;
4400	9391	14375	1	2.0E-78	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4790	9774	14759	6.31	2.0E-78	AW876618.1	EST_HUMAN	QV3-QT0028-220300-132-b11 OT0028 Homo sapiens cDNA
4173	9168	14165	5.78	1.0E-78	D63874.1	NT	Human mRNA for HMG-1, complete cds
4173	9168	14156	6.78	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
187	5250	10281	3.03	8.0E-77	R83144.1	EST_HUMAN	yp11h02.11 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:187155 5' similar to SP:ANKB_HUMAN_Q01484 ANKYRIN, BRAIN VARIANT 1;
4391	9382	14384	1.16	8.0E-77	BF206181.1	EST_HUMAN	6018866926F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109503 5'
1889	6878	11888	1.62	7.0E-77	AA625795.1	EST_HUMAN	zu91901.11 Soares testis_NH7 Homo sapiens cDNA clone IMAGE:745392 3'
2345	7319	12439	9.62	7.0E-77	4505944.1	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kd) (POLR2E) mRNA
2345	7319	12440	9.62	7.0E-77	4505944.1	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kd) (POLR2E) mRNA
280	6319	10329	5.1	6.0E-77	4504600	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1511	6509	11686	2.09	6.0E-77	A120468.1	EST_HUMAN	q877h12.11 Soares fetal lung NbHL19W Homo sapiens cDNA clone IMAGE:1745683 3'
4772	9756	14743	0.98	6.0E-77	4557752	NT	Homo sapiens midline 1 (Otp/BBB syndrome) (MID1) mRNA
4772	9756	14744	0.98	6.0E-77	4557762	NT	Homo sapiens midline 1 (Otp/BBB syndrome) (MID1) mRNA
1216	6215	11265	1.5	5.0E-77	AF041015.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1343	6340	11391	2.76	5.0E-77	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2613	7575	12689	1.11	5.0E-77	AF162668.1	NT	Homo sapiens fousid-like kinase 1 (TLK1) mRNA, complete cds
2680	7648	12762	1.24	5.0E-77	4503160	NT	Homo sapiens cullin 1 (CUL1) mRNA
3443	8451	13478	1.75	5.0E-77	8394518	NT	Homo sapiens ubiquitin specific protease 18 (USP18) mRNA
4565	9553	14539	0.99	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3) mRNA
4565	9553	14540	0.99	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3) mRNA
4780	9764	14749	2.68	5.0E-77	AL043953.1	EST_HUMAN	DKFZp434G1728_r1_494 (synonym: hesc3) Homo sapiens cDNA clone DKFZp434G1728 5'
3620	8627	13634	1.93	4.0E-77	AL449758.1	EST_HUMAN	AL449758 Homo sapiens fetal brain (Stavridis GS) Homo sapiens cDNA
1928	6914	12010	1.57	3.0E-77	5730039	NT	Homo sapiens SET domain and mariner transposase fusion gene (SEITMAR) mRNA
1928	6914	12011	1.57	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SEITMAR) mRNA
1334	6332	11380	2.09	2.0E-77	AV764617.1	EST_HUMAN	AV764617 MDS Homo sapiens cDNA clone MDSBT1F10 5'
1407	6405	11464	7.17	2.0E-77	AW987712.1	EST_HUMAN	RC3-BN0053-170200-011-01 BN0053 Homo sapiens cDNA
2045	7027	12138	6.42	2.0E-77	7706315	NT	Homo sapiens CGI-78 protein (LOC51634) mRNA
2618	7773	12602	2.22	2.0E-77	AB037838.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2518	7773	12603	2.22	2.0E-77	AB037838.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds

Page 135 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3922	8922	13913	1.53	2.0E-77	BE044316.1	EST_HUMAN	h�3b5.x1 Sorens_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10284 RETROVIRUS-RELATED GAG POLYPROTEIN;
4288	9280	14288	0.82	2.0E-77	AI613519.1	EST_HUMAN	h�22g2.x1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2280468 3' similar to TR:O85245 O65245_F21E10.7 PROTEIN;
4288	9280	14269	0.82	2.0E-77	AI613519.1	EST_HUMAN	h�22g2.x1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2280468 3' similar to TR:O85245 O85245_F21E10.7 PROTEIN;
4465	9455		1.29	2.0E-77	45040688_NT		Homo sapiens glutamin-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
4623	8608	14696	6.49	2.0E-77	AA653025.1	EST_HUMAN	ns65g12.61 NCI_CGAP_P72 Homo sapiens cDNA clone IMAGE:1188638 similar to SW:RL29_HUMAN P47814_60S_RIBOSOMAL PROTEIN L28. [1];contains element M8811 repetitive element;
44	5124	10112	0.89	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
44	5124	10113	0.89	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
270	5328	10340	3.11	1.0E-77	4502166_NT		Homo sapiens amyloid beta (A4) precursor protein (protease neprin-1), Alzheimer disease) (APP), mRNA
270	5328	10341	3.11	1.0E-77	4502168_NT		Homo sapiens amyloid beta (A4) precursor protein (protease neprin-1), Alzheimer disease) (APP), mRNA
884	7733	10925	6.09	1.0E-77	4502168_NT		Homo sapiens amyloid beta (A4) precursor protein (protease neprin-1), Alzheimer disease) (APP), mRNA
864	7733	10926	6.08	1.0E-77	4502168_NT		Homo sapiens amyloid beta (A4) precursor protein (protease neprin-1), Alzheimer disease) (APP), mRNA
1875	6884	11953	1.58	1.0E-77	AW056119.1	EST_HUMAN	lw83e016.x1 Sorens_thymus_NHFT Homo sapiens cDNA clone IMAGE:2536160 3'
2376	7348	12469	1.33	1.0E-77	AB029124.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
2871	7889	13002	2.25	1.0E-77	4503300_NT		Homo sapiens 2,4-dienyl COA reductase 1, mitochondrial (DECR1), mRNA
4227	9221	14201	4.08	1.0E-77	7706289_NT		Homo sapiens C51-50 protein (LOC511626), mRNA
4293	9384	14366	17.29	1.0E-77	AJ228041.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4516	9506	14486	2.27	1.0E-77	6552322_NT		Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BROA1-exon4, mRNA
4654	9542	14527	0.74	1.0E-77	AJ273014.1	EST_HUMAN	q103g04.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1981110 3'
4728	8713	14698	1.24	1.0E-77	11418424_NT		Homo sapiens collagen, type XI, alpha 1 (COL12A1), mRNA
4898	9877	14845	1.42	1.0E-77	7661849_NT		Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
4898	9877	14846	1.42	1.0E-77	7661849_NT		Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
4989	9361	14341	0.68	1.0E-77	4758053_NT		Homo sapiens cAMP responsive element binding protein 1 (CREB1), mRNA
84	5181	10172	2.26	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
84	5181	10173	2.26	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3240	8253	15274	0.88	6.0E-78	BF344101.1	EST_HUMAN	602016926511 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4152511 5'
217	5280	102891	1.01	5.0E-78	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
2491	7459	12574	4.77	5.0E-78	AW673424.1	EST_HUMAN	ba54h03_Y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800405 5' similar to WP:Y48B6A.6 CE22121
3301	8312	13339	4.18	5.0E-78	M55586.1	NT	Human collagenase type IV (COL4A4) gene, exon 6
1120	6126	11156	1.66	4.0E-78	AL043314.2	EST_HUMAN	DKFZp434N0323_r1_434 (synonym: hesc), Homo sapiens cDNA clone DKFZp434N0323 5'
1487	8484	11639	1.28	4.0E-78	AL355841.1	NT	Novel human gene mapping to chromosome 22
2254	7231	12350	20.59	4.0E-78	AF107405.1	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4195	9188	14168	1.87	4.0E-78	7656876	NT	Homo sapiens synctin (LOC30846), mRNA
4628	9613	14602	1.75	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4628	8613	14603	1.75	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
160	6226	10236	3.27	3.0E-78	AF095801.1	NT	Homo sapiens PIKFYVE gene, complete cds
160	6226	10236	3.27	3.0E-78	AF095801.1	NT	Homo sapiens PIKFYVE gene, complete cds
2240	7217	12335	1.06	3.0E-78	4502142	NT	Homo sapiens apoptosis inhibitor 3 (API3) mRNA
3142	8188	13180	1.34	3.0E-78	4507164	NT	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
3678	8683	1233	3.0E-78	AU140804.1	EST_HUMAN	AU140804 PLACE3 Homo sapiens cDNA clone PLACE300373 5'	
3048	8065		2.47	2.0E-78	U04488.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
3807	8907		1.51	2.0E-78	AA311672.1	EST_HUMAN	EST182553 Jurkat T-cells VI Homo sapiens cDNA 5' end
5007	8978	14953	1.22	1.0E-78	4758843	NT	Homo sapiens nucleophth 155kD (NUP155) mRNA
4560	9568	14533	3.85	9.0E-78	11525891	NT	Homo sapiens peptide YY (PYY), mRNA
4714	8699	14684	5.84	9.0E-78	BE000837.1	EST_HUMAN	RC2-BN0074-080300-014-012 BN0074 Homo sapiens cDNA
3857	8663	13668	0.91	8.0E-79	AL165210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4366	8257	14337	1.57	8.0E-79	D28476.1	NT	Human mRNA for KIAA0465 gene, complete cds
4366	8357	14338	1.57	8.0E-79	D28476.1	NT	Human mRNA for KIAA0465 gene, complete cds
3179	8195	13218	19.1	7.0E-79	BE619648.1	EST_HUMAN	6014726671 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875657 3'
3103	8119		0.98	4.0E-79	88222325	NT	Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA
311	5366	10377	1.61	3.0E-79	AF114488.1	NT	Homo sapiens Interseclin short isoform (ITSN) mRNA, complete cds
983	5978	11012	5.56	3.0E-79	AF232708.1	NT	Homo sapiens cell-line Ia8201a chloride ion current inducer protein (Cl ⁻) gene, complete cds
3025	8042	13051	2.52	3.0E-79	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
285	5343		1.02	2.0E-79	H63129.1	EST_HUMAN	Y48f03_51 Scares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:208541 3
628	5656	10661	1.22	2.0E-79	BE378928.1	EST_HUMAN	601159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 5'
815	5831	10986	1.47	2.0E-79	4757841	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA
1018	6028		1.19	2.0E-79	A1523747.1	EST_HUMAN	Y18f07_x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2118685 3'
1755	6745	11824	0.92	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1761	8745	11825	0.92	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
2087	7098	12180	3.3	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2087	7068	12181	3.3	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2130	7110	12223	2.05	2.0E-79	A_1271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
2249	7226	12346	2.65	2.0E-79	A_2744138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
4041	8027	14027	1.34	2.0E-78	A_1271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
3073	8089	13102	18.41	9.0E-80	AA725648.1	EST_HUMAN	ai23e05.st1 Soares testis NHT Homo sapiens cDNA clone 1343648 3'
3073	8089	13103	18.41	9.0E-80	AA725648.1	EST_HUMAN	ai23e05.st1 Soares testis NHT Homo sapiens cDNA clone 1343648 3'
3521	8528		1.06	8.0E-80	UB4387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
4797	9781	14164	1.67	7.0E-80	HO4619.1	EST_HUMAN	Y49e02.r1 Soares placenta NB2HP Homo sapiens cDNA clone MAGE:152067 5'
889	56007	10947	2.22	6.0E-80	AK122197.1	EST_HUMAN	h58d02.y1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16785 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR;
1604	68500	11981	2.05	6.0E-80	UB4388.1	NT	Homo sapiens NRD convertase mRNA, complete cds
2234	7211	12327	4.78	6.0E-80	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
2234	7211	12328	4.78	6.0E-80	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4162	9157	14142	1.33	6.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
4162	9157	14143	1.33	6.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
583	5614	10814	5.48	5.0E-80	4506228	NT	Homo sapiens proteosome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
825	5845	10882	1.83	5.0E-80	AF08830.1	NT	Homo sapiens serine-threonine protein kinase (MNKH) mRNA, complete cds
825	5845	10883	1.83	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNKH) mRNA, complete cds
1169	6172		1.23	5.0E-80	X91647.1	NT	H. sapiens nov1 gene (exon 12)
1428	6426		1.63	5.0E-80	AL1631283.2	NT	Homo sapiens chromosome 21, segment Hs21C089
2300	7275	12394	1.18	5.0E-80	UB9358.1	NT	Human l(3imb) protein homolog mRNA, complete cds
2363	7337	12454	8.73	5.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2722	7679	12792	6.28	5.0E-80	4504282	NT	Homo sapiens H3 histone family, member J (H3fJ) mRNA
4798	9780	14783	1.24	5.0E-80	AL1631288.2	NT	Homo sapiens chromosome 21, segment Hs21C068
216	5279		15.21	3.0E-80	AL1631281.2	NT	Homo sapiens chromosome 21, segment Hs21C010
4571	9559	14548	1.41	3.0E-80	BF085009.1	EST_HUMAN	PM0-GN001B-040900-002-E03 GN001B Homo sapiens cDNA
4753	9738		7.56	3.0E-80	BE817465.1	EST_HUMAN	Q14-BN0263-040860-241-g10 BN0263 Homo sapiens cDNA
1762	6754	11839	3.95	2.0E-80	R35321.1	EST_HUMAN	Y883608.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:380650 5'
1823	6813	11807	1.48	2.0E-80	AI444821.1	EST_HUMAN	RE74B7 subtracted retina cDNA library Homo sapiens cDNA clone RET4B7
2002	6985	12089	3.58	2.0E-80	AI0431162	EST_HUMAN	DK7Zp134D1323_r1 434 (synonym: hts3) Homo sapiens cDNA clone DK7Zp134D1323 5'

Page 138 of 209
Table 4
Single Exon Probes Expressed in

Single Exon Probes Expressed in HBL100 Cells						
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source
338	6390			1.78	1.0E-80 AL163303.2	NT
781	5812	10842		1.53	1.0E-80 AF231920.1	NT
1814	6900			2.27	1.0E-80 AI732568.1	EST_HUMAN
4674	9859	14642		0.85	1.0E-80 NR9520.1	EST_HUMAN
2144	7123	12239		0.95	7.0E-81 AA011080.1	EST_HUMAN
4262	9285	14244		6.63	6.0E-81 BE256289.1	EST_HUMAN
4262	9255	14245		6.63	6.0E-81 BE256289.1	EST_HUMAN
2155	7134	12253		5.18	5.0E-81 BE268042.1	EST_HUMAN
1786	6778	11870		1.6	4.0E-81 AW778612.1	EST_HUMAN
3087	8113	13131		3.68	4.0E-81 AB037766.1	NT
3544	8551	13558		0.78	4.0E-81 AW004080.1	EST_HUMAN
4036	9032	14019		2.04	4.0E-81 AF283308.1	EST_HUMAN
4036	8032	14020		2.04	4.0E-81 AF263308.1	NT
4268	9281	14251		0.99	4.0E-81 89232091	NT
1248	6246	11285		12.27	3.0E-81 Y18000.1	EST_HUMAN
1248	6246	11286		12.27	3.0E-81 Y18000.1	NT
2310	7285	12015		1.5	3.0E-81 AF077188.1	NT
2922	7941	12257		6.98	3.0E-81	4506280
2922	7941	12958		5.68	3.0E-81	4506280
2759	7780	12804		2.23	2.0E-81 BE784638.1	EST_HUMAN
2759	7780	12805		2.23	2.0E-81 BE784638.1	EST_HUMAN
3686	8690	13693		0.93	2.0E-81 AW616542.1	EST_HUMAN
3568	8575	13581		1.35	1.0E-81 AW960658.1	EST_HUMAN
4384	8375	14354		2.11	1.0E-81 AA040370.1	EST_HUMAN
4510	8690	14479		10.97	1.0E-81 BE04798681	EST_HUMAN

Page 139 of 209
Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13	5093	10077	4.69	8.0E-82	AF161406.1	NT	Homo sapiens HSPC2288 mRNA, partial cds
107	5093	10077	5.28	8.0E-82	AF161406.1	NT	Homo sapiens HSPC2288 mRNA, partial cds
261	5320	10330	2.55	8.0E-82	U05988.1	NT	Human CRFB4 gene, partial cds
804	5825	10855	2.38	8.0E-82	U05988.1	NT	Human CRFB4 gene, partial cds
876	5894	10835	1.93	8.0E-82	U05988.1	NT	Human CRFB4 gene, partial cds
1459	6466	11515	1.39	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1817	6614	11681	1.23	8.0E-82	8716601	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4121	9116	14102	0.84	8.0E-82	8923492	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
1424	6421		1.04	7.0E-82	BF035327.1	EST_HUMAN	601458531F NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3862086 5'
2693	7651	12795	1.55	7.0E-82	AU144050	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3'
1632	6829	11698	1.00	3.4E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
275	5334	10347	16.31	3.0E-82	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-1, Alzheimer disease) (APP), mRNA
693	5717	10734	3.65	3.0E-82	BE0050705.1	EST_HUMAN	RC22-BN0120-010400-013-012 BN0120 Homo sapiens cDNA
779	5800	10830	6.3	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
859	5878	10919	8.88	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-1, Alzheimer disease) (APP), mRNA
1044	6054		80.59	3.0E-82	AA725648.1	EST_HUMAN	el223e05_s1_Serres_Ieslisi_NHT Homo sapiens cDNA clone 1342848 3'
1337	6335	11385	0.98	3.0E-82	AW876073.1	EST_HUMAN	RC6-PT0001-180100-021-B02 PT0001 Homo sapiens cDNA
1438	6435	11482	2.02	3.0E-82	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1860	6849	11937	1.66	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN0005-260700-018-904 BN0005 Homo sapiens cDNA
3198	8214		2.15	3.0E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), mRNA
592	5823	10821	1.39	2.0E-82	AB025216.1	NT	Homo sapiens mRNA for KIAA0986 protein, partial cds
592	5823	10822	1.39	2.0E-82	AB025216.1	NT	Homo sapiens mRNA for KIAA0986 protein, partial cds
1647	6843	11715	1.78	2.0E-82	AL046390.1	EST_HUMAN	DKFZp43M117_r1434 (synonym: hies2) Homo sapiens cDNA clone DKFZp43M117 6'
3756	8759	13158	0.85	2.0E-82	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4112	9106	14092	0.83	2.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), mRNA
4428	8416	14403	1.06	2.0E-82	AB029018.1	NT	Homo sapiens mRNA for KIAA1086 protein, partial cds
4426	8416	14404	1.06	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1086 protein, partial cds
4720	8705	14891	2.77	2.0E-82	AF045555.1	NT	Homo sapiens replication factor C subunit 2 (RFC2) gene, complete cds
4908	9887	14859	1.68	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
4908	9887	14860	1.98	2.0E-82	4507680	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6) mRNA

Page 140 of 209

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
587	5616	10616	1.67	1.0E-82	115456921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDAS), mRNA
1189	6180		1.57	1.0E-82	BE885106.1	EST_HUMAN	601510859F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207 5'
1266	6264	11305	3.2	1.0E-82	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f010 BT0310 Homo sapiens cDNA
1267	6265	11306	1.14	1.0E-82	AB01110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
1389	6386	11438	4.62	8.0E-83	BE385973.1	EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:36114362 5'
1642	7700	11709	4.3	8.0E-83	N68951.1	EST_HUMAN	2248112.st1 Soares fetal liver spleen INF-S Homo sapiens cDNA clone IMAGE:2856823 3'
1339	6337	11386	1.67	7.0E-83	AW385529.1	EST_HUMAN	QV4-L70016-271289-06B-h11 LT0016 Homo sapiens cDNA
2784	7814		1.62	7.0E-83	AA584855.1	EST_HUMAN	no1201.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:11004497 3' similar to contains Ali repetitive element;
4670	8655		6.92	7.0E-83	BF221813.1	EST_HUMAN	TP37a07.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:38477893 3' similar to TR:Q9Y316 Q9Y316
5036	10097			1.51	7.0E-83	BF221813.1	EST_HUMAN
401	5437	10456		1.97	6.0E-83	M33320.1	NT
1749	6743	11822	7.97	6.0E-83	AW573088.1	EST_HUMAN	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
2977	7985			1.02	6.0E-83	AF231919.1	NT
2988	8014	13026	1.01	6.0E-83	AA701457.1	EST_HUMAN	SW:YBEB_HAEIN_P44471_HYPOTHETICAL PROTEIN H10034. ;
3483	8191	13507	0.82	6.0E-83	11430241	NT	Homo sapiens chromosome 21 unknown mRNA
932	5649		1.95	6.0E-83	U17883.1	NT	Human hypothetical protein FJ_10379 (FJ_10379). mRNA
1697	7704			2.65	6.0E-83	AF006305.1	NT
3553	8560	13566	1.13	5.0E-83	AL133207.2	NT	Homo sapiens 26S proteasome regulatory subunit (S1U23), mRNA, complete cds
3810	6813	13819	0.99	5.0E-83	48885180	NT	Novel human gene mapping to chromosome X
4907	9886	14857	14.02	5.0E-83	4557013	NT	Homo sapiens deoxribonuclease (DNASE), mRNA
4907	9886	14858	14.02	5.0E-83	4557013	NT	Homosapiens database (CAT) mRNA
634	6662	10667	1.76	4.0E-83	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3435	8443	13469	1.08	4.0E-83	BE888078.1	EST_HUMAN	601511560F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913185 5'
982	5997		3.78	3.0E-83	AA388311.1	EST_HUMAN	EST778542 Placenta I Homo sapiens cDNA similar to endogenous retrovirus ERV9
2705	7682		1.44	3.0E-83	AA332654.1	EST_HUMAN	np8/c07.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR.12 THR repetitive element;
1764	6756	11841	1.7	2.0E-83	AA4983492.1	EST_HUMAN	Q92814 MYELOBLAST KIAA0216. ;

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1784	6756	11842	1.7	2.0E-83	AA993492.1	EST_HUMAN	Orf64905_s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614
1884	6873	11862	3.01	2.0E-83	N66851.1	EST_HUMAN	Orf82614 MYEOBLAST KHA0216. ;
2779	7800	12818	2.73	2.0E-83	BE828694.1	EST_HUMAN	2848f12-61 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:285823 3'
3195	8211		2.22	2.0E-83	11430834 NT	EST_HUMAN	RCG-E10046-280860-013-H12 ET0046 Homo sapiens cDNA
3687	8691		0.74	2.0E-83	AL183202.2	NT	Homo sapiens sal (Drosophila)like 1 (SALL1), mRNA
4210	9203	14185	4.16	2.0E-83	AF20219.1	NT	Homo sapiens chromosome 21 segment HS21CQ02
4517	9507	14487	6.32	2.0E-83	7706398 NT	Hom sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds	
4517	9507	14498	6.32	2.0E-83	7706398 NT	Hom sapiens ankyrin repeat-containing protein ASB-2 (LOC51876), mRNA	
1387	6384	11495	2.31	1.0E-83	4504326 NT	Hom sapiens hydroxyacyl-Coenzyme A thiolesterase/enoyle-Coenzyme A thiolesterase/enoyle-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHb) mRNA	
1387	6384	11436	2.31	1.0E-83	4504326 NT	Hom sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketacyl-Coenzyme A thiolesterase/enoyle-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHb) mRNA	
2585	7548	12863	1.22	1.0E-83	BE828690.1	EST_HUMAN	601607375f1 NIH MGC_71 Homo sapiens cDNA clone IMAGE:3808754 5'
3777	8780	13783	6.31	1.0E-83	AF063768.1	NT	Rattus norvegicus brain specific contactin-binding protein CBP80 mRNA, partial cds
4122	9116	14103	3.74	1.0E-83	225822.1	NT	H.sapiens gene for mitochondrial dodecenoyl-CoA delta-isomerase, exon 3
4733	9718	14703	2.36	1.0E-83	4502166 NT	Hom sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA	
3707	8711	13714	4.14	7.0E-84	BE801209.1	EST_HUMAN	60167623f1 NIH MGC_71 Homo sapiens cDNA clone IMAGE:3858853 5'
1276	6274	11313	2.87	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-201600-011-g05 FN0119 Homo sapiens cDNA
1276	6274	11314	2.87	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-201600-011-g05 FN0119 Homo sapiens cDNA
2334	7308	12429	3.11	6.0E-84	AA776574.1	EST_HUMAN	aa868a03_s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
5044	10015	14984	0.98	6.0E-84	RO5659.1	EST_HUMAN	je83e04.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125282 5'
704	6728	10745	0.8	6.0E-84	AA382811.1	EST_HUMAN	EST86094 Testis 1 Homo sapiens cDNA 5' end
2945	7984		1.24	6.0E-84	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1386	6383	11434	2.71	4.0E-84	AI685321.1	EST_HUMAN	wa76c-04-x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW_NRDC_HUMAN_O3847_NARDILYSIN PRECURSOR ;
4782	9776	14780	1.83	4.0E-84	4505928 NT	Hom sapiens polymerase (DNA-directed), alpha (70RD) (POLA2), mRNA	
4783	9777	14781	1.73	4.0E-84	AF069601.2	NT	Hom sapiens myosin light chain kinase isoform 2 (MLCK), mRNA, complete cds
314	5369	10380	1.77	3.0E-84	AF026200.1	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
1920	6908	12000	1.89	3.0E-84	5453885 NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA	
1958	6944	12046	3.99	3.0E-84	AI096880.1	NT	Nova human mRNA containing Zinc finger C2H2 type domains
3510	8518	13229	0.97	3.0E-84	AB028698.1	NT	Homo sapiens DNA, DLECI to ORCTL4 gene region, section 1/2 (DLECI, ORCTL3, ORCTL4 genes, complete cds)

Page 142 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3652	8667	13873	5.61	3.0E-84	AF014459.1	NT	Human sapiens X-linked juveniles retinoblastoma precursor protein (XLRS1) mRNA, complete cds
2047	7029	12141	4.68	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0786-180600-272-508_BT0785 Homo sapiens cDNA
2047	7029	12142	4.68	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0786-180600-272-508_BT0785 Homo sapiens cDNA
2873	7892	12915	8.83	2.0E-84	AF036943.1	NT	Human sapiens myelin transcription factor 1-like (MFT1-1) mRNA, complete cds
2892	7911	12932	1.41	2.0E-84	X89211.1	NT	Human sapiens DNA for endogenous retrovirus like element
310	6385	10376	1.21	1.0E-84	AF114488.1	NT	Human sapiens tyrosine 3-monooxygenase triphosphatase 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
545	5579	10583	16.88	1.0E-84	4507952	NT	Human sapiens intersects short isoform (TSN) mRNA, complete cds
710	6734	1123	1.0E-84	11427631	NT	Human sapiens complement component 5 (C5) mRNA	
1274	6272	11311	2.78	1.0E-84	AA98439.1	EST_HUMAN	lrm85611_s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1628885 3'
2001	6984	12098	1.8	1.0E-84	BE392337.1	EST_HUMAN	60130806F NIH MGIC 44 Homo sapiens cDNA clone IMAGE:3626257 5'
2162	7141	12288	1.8	1.0E-84	11427197	NT	Human sapiens per centihour material 1 (PCM1) mRNA
3685	8870	13875	2.55	1.0E-84	AA20351.1	EST_HUMAN	nw12e08_st NCI CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239106 3'
4282	9284	14271	4.33	1.0E-84	AJ228041.1	NT	Human sapiens 859 kb config between AML1 and CBR1 on chromosome 21q22; segment 1/3
4561	9549	14534	2.83	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_1_434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434N0323 5'
4581	9559	14535	2.83	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_1_434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434N0323 5'
4756	9284	14271	2.67	1.0E-84	AJ228041.1	NT	Human sapiens 859 kb config between AML1 and CBR1 on chromosome 21q22; segment 1/3
4852	8929	14907	0.71	1.0E-84	AW371947.1	EST_HUMAN	RC4-BT0311-141289-012-906 BT0311 Homo sapiens cDNA
4952	8929	14908	0.71	1.0E-84	AW371947.1	EST_HUMAN	RC4-BT0311-141289-012-906 BT0311 Homo sapiens cDNA
952	5968		2.75	9.0E-85	AL163209.2	NT	Human sapiens chromosome 2 segment HS21C009
1056	6085	11094	10.8	9.0E-85	U51432.1	NT	Human sapiens nuclear protein Skp mRNA, complete cds
1056	6085	11095	10.8	9.0E-85	U51432.1	NT	Human sapiens nuclear protein Skp mRNA, complete cds
1543	6541	11598	1.1	9.0E-85	MS3282.1	NT	Human Plasminogen gene, exon 7
1543	6541	11599	1.1	9.0E-85	MS3282.1	NT	Human Plasminogen gene, exon 7
1635	6632	11702	2.05	9.0E-85	7657020	NT	Human sapiens DKKZp434P211 protein (DKFZp434P211) mRNA
3711	8715	13717	0.91	9.0E-85	7019418	NT	Human sapiens chitosanase (HUMAUANT1G) mRNA
4130	9125	14109	1.08	9.0E-85	AL163280.2	NT	Human ornithine decarboxylase 21 segment HS21C080
4639	9824	14815	1.44	9.0E-85	N33764.1	NT	Human ornithine decarboxylase gene, complete cds
4639	9824	14816	1.44	9.0E-85	N33764.1	NT	Human ornithine decarboxylase gene, complete cds
4757	9741	14728	1.1	9.0E-85	AL163288.2	NT	Human sapiens chromosome 21 segment HS21C088
1119	6125	11155	34.29	7.0E-85	LO5094.1	NT	Human sapiens ribosomal protein L27 mRNA, complete cds
2271	7247	12384	2.11	6.0E-85	AL163284.2	NT	Human sapiens chromosome 21 segment HS21C084
1280	6279	11320	0.77	3.0E-85	AF086157.1	NT	Human sapiens protein phosphatase 2A B gamma subunit gene, exon 6
1742	6737	11813	6.32	3.0E-85	T87495.1	EST_HUMAN	ye53g09.1 Scores fetal liver spliced 1NFLS Homo sapiens cDNA clone IMAGE:121504 6'

Page 143 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4188	9181	14164	1.26	3.0E-85	BE287189.1	EST_HUMAN	601189704F2_NIH_MGC_7_Homo sapiens cDNA clone IMAGE:3533616 5'
4743	9728	14714	1.48	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4743	9728	14715	1.48	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4809	9793	14775	1	3.0E-85	7363442	NT	Homo sapiens olfactory receptor, family 12, subfamily D, member 2 (OR12D2), mRNA
948	6984	10988	0.72	2.0E-85	7657268	NT	Homo sapiens KIAA0829 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0829), mRNA
1023	6033	11084	1.98	2.0E-85	AF248550.1	NT	Homo sapiens Intersectin 2 (SH3D1B), mRNA, complete cds
1380	6377	11425	1.33	2.0E-85	7706205	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA
1395	6392	11445	7.52	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2), mRNA
1395	6392	11446	7.52	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2), mRNA
2169	7148	12285	1.4	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2750	6316		10.24	2.0E-85	7657468	NT	Homo sapiens similar to integral membrane glycoprotein POM121 (POM121L1), mRNA
2958	7975	12980	2.18	2.0E-85	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4207	9200	14182	5.76	2.0E-85	45058880	NT	Homo sapiens plasminogen (PLG), mRNA
4755	9740	14725	0.97	2.0E-85	AL163264.2	NT	Homo sapiens chromosomal segment HS21C084
2223	7200		3.19	1.0E-85	BE794306.1	EST_HUMAN	6011591416F1_NIH_MGC_7_Homo sapiens cDNA clone IMAGE:3945618 5'
2328	7303	12423	5.67	1.0E-85	BE618392.1	EST_HUMAN	601462817F1_NIH_MGC_67_Homo sapiens cDNA clone IMAGE:3866021 5'
2328	7303	12424	5.97	1.0E-85	BE618392.1	EST_HUMAN	601462817F1_NIH_MGC_67_Homo sapiens cDNA clone IMAGE:3866021 5'
1404	6401		64.78	9.0E-86	BE274217.1	EST_HUMAN	601120778F1_NIH_MGC_20_Homo sapiens cDNA clone IMAGE:2987680 5'
923	5940	10972	0.75	7.0E-86	AA8650801.1	EST_HUMAN	601462817F1_NIH_MGC_67_Homo sapiens cDNA clone IMAGE:1403559 3'
923	5940	10973	0.75	7.0E-86	AA8650801.1	EST_HUMAN	601462817F1_NIH_MGC_67_Homo sapiens cDNA clone IMAGE:1403559 3'
1275	6273	11312	2.27	6.0E-86	4505492	NT	Homo sapiens oxoglutarate dehydrogenase (lipoyamide) (GCDH) mRNA
5001	9872	14848	1.8	6.0E-86	8605633	NT	Homo sapiens 24 kDa intrinsic membrane protein (PMP24), mRNA
211	5274	10288	1.35	4.0E-86	BE547173.1	EST_HUMAN	601072584F1_NIH_MGC_12_Homo sapiens cDNA clone IMAGE:3458830 5'
264	5323	10332	2.04	2.0E-86	AA305264.1	EST_HUMAN	EST177232 Jurkat T-cells VI Homo sapiens cDNA 5' end
411	6448		2.83	2.0E-86	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C03
1170	6173	11207	1.94	2.0E-86	NT	EST_HUMAN	
2128	7108	12222	3.37	2.0E-86	8635487	NT	Human endogenous retrovirus, complete genome
2207	7184	12307	1.08	2.0E-86	AB033103.1	NT	Homo sapiens mRNA for KIAA1277 protein, partial cds
3331	8341	13359	1.19	2.0E-86	AW868142.1	EST_HUMAN	EST378215 IMAGE: resequences, MAGI Homo sapiens cDNA
3661	8666	13871	2.84	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta), mRNA, complete cds
3661	8666	13872	2.84	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-kappa (LPAAT-kappa), mRNA, complete cds
3927	8927		2.69	2.0E-86	AW616742.1	EST_HUMAN	hbbtgbx1 NCI CGAP_916 Homo sapiens cDNA clone IMAGE:2810542 3'
4645	8630	14625	3.42	2.0E-86	AF056190.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A), mRNA, partial cds

Page 144 of 209
Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1562	6559	11621	2.08	1.0E-86	4826655	NT	Human sapiens NADH dehydrogenase (ubiquinone) F-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA
3089	8105	13120	1.45	1.0E-86	6453849	NT	Human sapiens fibulin 5 (FBLN5) mRNA
3164	8180	13202	2.68	1.0E-86	1204921	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3222	8237	13258	1.17	1.0E-86	AL163209.2	NT	Human sapiens chromosome 21 segment HS21C009
3222	8237	13259	1.17	1.0E-86	AL163209.2	NT	Human sapiens chromosome 21 segment HS21C009
3842	8844	13852	1.22	1.0E-86	7706161	NT	Human sapiens hypothetical protein (LOC51318) mRNA
3842	8844	13853	1.22	1.0E-86	7706161	NT	Human sapiens hypothetical protein (LOC51318) mRNA
4142	9137	14121	5.37	1.0E-86	AL163300.2	NT	Human sapiens chromosome 21 segment HS21C100
476	5512	10525	131.14	9.0E-97	X62245.1	NT	O.uncinata mRNA for elongation factor 1 alpha
2233	7210	12325	1.89	7.0E-97	BF063211.1	EST_HUMAN	7h85102_x1_NCI_CGAP_Co8_Homo sapiens cDNA clone IMAGE:3322778.3'
2233	7210	12326	1.98	7.0E-97	BF063211.1	EST_HUMAN	7h85102_x1_NCI_CGAP_Co16_Homo sapiens cDNA clone IMAGE:3322779.3'
3448	8456	13482	0.78	6.0E-97	7657213	NT	Human sapiens hormonally upregulated neu tumor-associated kinase (HUNK) mRNA
1140	6145	11176	2.38	5.0E-97	AA392811.1	EST_HUMAN	EST:96084 Testis Homo sapiens cDNA 5' end
951	5987	11000	1.12	4.0E-97	AL163210.2	NT	Human sapiens chromosome 21 segment HS21C010
1153	6157	11180	18.02	4.0E-97	AB037835.1	NT	Human sapiens mRNA for KIAA1414 protein, partial cds
1980	6985	12071	1.85	4.0E-97	AB007925.1	NT	Human sapiens mRNA for KIAA0486 protein, partial cds
2355	7329	12444	1.2	4.0E-97	7706289	NT	Human sapiens CGI-60 protein (LOC51629) mRNA
2355	7329	12445	1.2	4.0E-97	7706289	NT	Human sapiens CGI-60 protein (LOC51629) mRNA
3383	8391	13414	1.88	4.0E-97	5174574	NT	Human sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLL4) mRNA
2704	7681	12773	5.54	2.0E-97	4885420	NT	Human sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA
2818	7897	1.17	2.0E-97	BF327920.1	EST_HUMAN	QVO-BN0148_Homo sapiens cDNA clone HEMBA1000307.6'	
3696	8700	13703	0.98	2.0E-97	AU116935.1	EST_HUMAN	AU116935_HEMBA1 Homo sapiens cDNA clone HEMBA1000307.6'
4758	9742	14727	0.66	2.0E-97	BF376311.1	EST_HUMAN	CMD-TN0038-150900-562-h08 TN0038_Homo sapiens cDNA
1163	7698		1.89	1.0E-87	7705683	NT	Human sapiens putative glycolipid transfer protein (LOC51054) mRNA
1406	8403	11460	1.69	1.0E-87	AW361977.1	EST_HUMAN	PM2-C10265-141058-001-g04 CT0265_Homo sapiens cDNA
1406	8403	11461	1.69	1.0E-87	AW361977.1	EST_HUMAN	PM2-C10265-141058-001-g04 CT0265_Homo sapiens cDNA
3528	8635	13640	13.27	1.0E-87	Y00052.1	NT	Human mRNA for T-cell cyclophilin
3649	8655	13861	2.3	1.0E-87	4758827	NT	Human sapiens neuredin III (NRXN3) mRNA
9019	5926	10961	0.7	9.0E-88	5453887	NT	Human sapiens protease inhibitor 4 (kallistatin) (PI4) mRNA
1089	6096	11126	6.3	9.0E-88	AF167465.1	NT	Human sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1331	6329	11377	2.48	9.0E-88	AB037820.1	NT	Human sapiens mRNA for KIAA1599 protein, partial cds
1331	6329	11378	2.48	9.0E-88	AB037820.1	NT	Human sapiens mRNA for KIAA1599 protein, partial cds

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3542	8549	13557	0.89	9.0E-88	AL163205.2	NT	Homo sapiens chromosome 21 segment HS21C009
4147	9142	14126	3.04	9.0E-88	X91928.1	NT	H. sapiens ECE-1 gene (exon 9)
4147	9142	14127	3.04	9.0E-88	X91928.1	NT	H. sapiens ECE-1 gene (exon 9)
1792	6783		1.98	5.0E-88	7681887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2568	7531	12650	4.62	5.0E-88	N88989.1	EST_HUMAN	K9710F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9710 5' similar to ZINC FINGER PROTEIN HFZ1
2831	7850	12867	0.71	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
2941	7860	12879	0.76	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
2941	7860	12880	0.76	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
3305	8316		2.66	5.0E-88	AI693217.1	EST_HUMAN	wd0808.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2333789 3' similar to contains Alu repetitive element; contains element MER22 MER22 repetitive element;
3498	8468	13493	0.7	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
1309	6307	11355	1.13	4.0E-88	BF091228.1	EST_HUMAN	PMI-TN0028-030900-004-f10 TN0028 Homo sapiens cDNA
1309	6307	11356	1.13	4.0E-88	BF091228.1	EST_HUMAN	PMI-TN0028-030900-004-f10 TN0028 Homo sapiens cDNA
722	5745	10764	1.4	3.0E-88	1154580	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634) mRNA
1776	6768		2.26	3.0E-88	4505020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
2877	7896	12920	4.85	3.0E-88	N68651.1	EST_HUMAN	zz44812.31 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:285623 3'
4118	9112	14086	0.69	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4118	9112	14087	0.69	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4351	9342		3.84	3.0E-88	11428300	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220) mRNA
1019	6029	11058	1.27	2.0E-88	7305198	NT	Homo sapiens Celsamillin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1585	6582	11644	1.92	2.0E-88	AF246218.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1711	6708	11782	4.8	2.0E-88	AF246218.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3884	8392	12416	0.99	2.0E-88	AF246218.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4301	9293	14280	2.35	2.0E-88	5031668	NT	Homo sapiens dynein, exon 1, light polypeptide 4 (DNAL4), mRNA
2861	7620	12732	1.49	8.0E-89	BE311657.1	EST_HUMAN	601142409F1 NIH MG-14 Homo sapiens cDNA clone IMAGE:3506186 5'
430	5468	10486	1.24	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
430	6469	10487	1.24	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
4730	9715	14700	3.49	7.0E-89	4657380	NT	Homo sapiens complement component 8, beta polypeptide (C8B) mRNA
4774	9758	14748	5.7	7.0E-89	AL045748.1	EST_HUMAN	DKFZp43E248_71434 (synonym: hts3) Homo sapiens cDNA clone DKFZp43E248 5'
1007	6017	11047	2.12	8.0E-89	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (IMMT), mRNA
2151	7130	12247	1.98	8.0E-89	4506124	NT	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4), mRNA
2368	7340	12456	5.05	8.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L_3 (UBE2L3) mRNA
2368	7340	12457	5.05	8.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L_3 (UBE2L3) mRNA

Page 146 of 209
Table 4

Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3446 8454	13480		0.75	6.0E-89	7661817	NT	Human sapiens HSPC159 protein (HSPC159), mRNA
4354 8345	14324		0.81	6.0E-89	7681737	NT	Human sapiens HSPC019 protein (HSPC019), mRNA
4503 8493	14470		3.9	6.0E-89	AB0078866.2	NT	Human sapiens mRNA for KIAA0408 protein, partial cds
4503 8493	14471		3.9	6.0E-89	AB0078866.2	NT	Human sapiens mRNA for KIAA0408 protein, partial cds
4903 9882	14852		3.31	6.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Bay1or-HGSC project=TCBA_Homo_sapiens cDNA clone TCBAP2E0383
4903 9882	14853		3.31	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Bay1or-HGSC project=TCBA_Homo_sapiens cDNA clone TCBAP2E0383
2807 7827	12843		0.95	3.0E-89	AW976181.1	EST_HUMAN	EST388280 MAGE gene sequences, MAGN_Homo_sapiens cDNA
127 6442	10482		0.87	2.0E-89	7706870	NT	Human sapiens PXR2b protein (PXR2b), mRNA
127 6442	10483		0.87	2.0E-89	7706870	NT	Human sapiens PXR2b protein (PXR2b), mRNA
526 6581	10584		0.68	2.0E-89	AB037763.1	NT	Human sapiens mRNA for KIAA1342 protein, partial cds
2811 7831	12847		1.44	2.0E-89	AI222095.1	EST_HUMAN	qp96c08_x1_Soares_NFL_T_GBC_S1_Homo_sapiens cDNA clone IMAGE:18430222 3' similar to gb_J04131 GAMMA GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element
4022 8018	14005		1.18	2.0E-89	AF089897.1	NT	Human sapiens topoisomerase-related function protein (TRF4-2), mRNA, partial cds
4030 8028	14014		4.76	2.0E-89	X58742.1	NT	H. sapiens HK3 gene for tyrosine kinase (PTK), exons 10-11
4030 8028	14015		4.76	2.0E-89	X58742.1	NT	H. sapiens HK3 gene for tyrosine kinase (PTK), exons 10-11
4223 9217	14198		1.09	2.0E-89	AL63203.2	NT	Human sapiens chromosome 21 segment HS21C003
4387 8359	14339		1.05	2.0E-89	AJ007378.1	NT	Human sapiens GOT gene, exon 5
1046 6058	11084		3.19	8.0E-90	AL163246.2	NT	Human sapiens chromosome 21 segment HS21C046
1047 6058	11084		2.72	8.0E-90	AL163246.2	NT	Human sapiens chromosome 21 segment HS21C046
1310 7744	11357		3.66	8.0E-90	BE810561.1	EST_HUMAN	7e3f6f08_x1_NCI_CGAP_Lu24_Homo_sapiens cDNA clone IMAGE:3284583 3'
1310 7744	11358		3.66	8.0E-90	BE810561.1	EST_HUMAN	7e3f6f08_x1_NCI_CGAP_Lu24_Homo_sapiens cDNA clone IMAGE:3284583 3'
826 5846			4.22	7.0E-90	AF223391.1	NT	Human sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2894 8012	13024		1.08	6.0E-90	X91923.1	NT	H. sapiens ECE-1 gene (exon 6)
2894 8012	13025		1.08	6.0E-90	X91926.1	NT	H. sapiens ECE-1 gene (exon 6)
4105 8099	14086		9.58	6.0E-90	8922398	NT	Human sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4105 8099	14086		9.58	6.0E-90	8922398	NT	Human sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
154 5220			78.69	5.0E-90	AB035344.1	NT	Human sapiens TCL8 gene, exon 1-10b
1173 6178	11210		2.39	5.0E-90	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds

Page 147 of 209

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1784	6776	11867	1.48	5.0E-90	AI222095.1	EST_HUMAN	gb96c08_x1 Scareas_NFL_1_GBC_S1_Homo_sapiens_cDNA_clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element
1784	6776	11868	1.48	5.0E-90	AI222095.1	EST_HUMAN	gb96c08_x1 Scareas_NFL_1_GBC_S1_Homo_sapiens_cDNA_clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element
2484	7452	12568	1.82	5.0E-90	AF114487.1	NT	Homo sapiens intersects long isoform (ISN) mRNA, complete cds
300	5357	10369	2.4	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21; unknown mRNA
300	5357	10370	2.4	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21; unknown mRNA
1070	6078	11109	3.28	4.0E-90	4505319	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYP1), mRNA
1650	6648	11719	9.18	4.0E-90	X86033.1	NT	H. sapiens gene encoding discoidin receptor tyrosine kinase, exon 18
4522	9512	14497	4.85	4.0E-90	DB7675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4653	9638	14629	1.95	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4673	9658	14641	1.82	4.0E-90	M95967.1	NT	Human prohormone converting enzyme (EC2) gene, exon 8
5010	9981	14956	0.92	4.0E-90	5728777	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
213	5276	10290	4.2	2.0E-90	BE5371913.1	EST_HUMAN	601087378F1 NIH_MGC_10_Homo_sapiens_cDNA_clone IMAGE:34538345'
1164	6168	11191	71.49	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nucleosome chromosomal) protein 17 (HMG17), mRNA
1154	6168	11192	71.49	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nucleosome chromosomal) protein 17 (HMG17), mRNA
3755	8758	13757	1.88	2.0E-90	AI138213.1	EST_HUMAN	qc54c02_x1 Scareas_placenta_8to9weeks_2NhhIPøN_Homo_sapiens cDNA clone IMAGE:17134103'
4650	9538	14524	0.97	2.0E-90	AB006827.1	NT	similar to SW:OLF3_MOUSE_P23275_Olfactory Receptor OR3.3;
4754	8739	14724	8.45	2.0E-90	5728855	NT	Homo sapiens mRNA for KIAA0289 gene, partial cds
274	5333	10346	5.3	1.0E-90	4502166	NT	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
373	7693	10436	1.88	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21; unknown mRNA
374	7693	10436	1.9	1.0E-90	AF231920.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
686	5710	10723	1.73	1.0E-90	AI237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
686	5710	10724	1.73	1.0E-90	AI237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
720	6743	10761	11.11	1.0E-90	AF264750.1	NT	Homo sapiens A1R-like protein mRNA, partial cds
720	5743	10762	11.11	1.0E-90	AF284750.1	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1083	6100		3	1.0E-90	4507828	NT	Homo sapiens protein phosphatase 2A_B gamma subunit gene, exon 3
1287	8286	11328	2.29	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A_B gamma subunit gene, exon 3
1287	8286	11330	2.29	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A_B gamma subunit gene, exon 3
1628	6625		4.57	1.0E-90	BE379894.1	EST_HUMAN	601169863F2 NIH_MGC_53_Homo_sapiens cDNA clone IMAGE:3511118 6'

Page 148 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1861	6850	11638	2.56	1.0E-90	11420514	NT	Homo sapiens similar to <i>SALL1</i> (sal (Drosophila)-like (LOC557187), mRNA
2780	7801	12819	9.3	1.0E-90	60065720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3761	8764	13765	0.99	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0503 protein, partial cds
3761	8764	13766	0.89	1.0E-80	AB020710.1	NT	Homo sapiens mRNA for KIAA0503 protein, partial cds
4289	9281	14278		1.62	1.0E-90	AF167340.1	Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
4073	9067	14057	6.67	8.0E-91	D12234.1	EST_HUMAN	HUMAN0005381 Liver HepG2 cell line, Homo sapiens cDNA clone s381 3'
3394	8402	13428	2.26	5.0E-91	AA7027194.1	EST_HUMAN	Zigzag04.st Soares fetal liver spleen INF1S_S1 Homo sapiens cDNA clone IMAGE:446015 3'
4385	9376	14355	1.19	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1020287 5'
4385	9376	14356	1.19	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1020287 5'
4664	8849	14636	1.09	6.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF6), mRNA
4664	8849	14637	1.09	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF6), mRNA
3129	8145	13165	1.87	4.0E-91	AF156376.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3129	8145	13166	1.87	4.0E-91	AF156376.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
1578	6575	11637	1.86	3.0E-91	11430193	NT	Homo sapiens solute carrier family 3 (SLC4A3), mRNA
1578	6575	11638	1.86	3.0E-91	11430193	NT	Homo sapiens solute carrier family 3 (SLC4A3), mRNA
1754	7701	11830	1.4	3.0E-91	AF265555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
3265	8278	13201	1.55	3.0E-91	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3380	8388	13410	3.62	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3380	8388	13411	3.62	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3699	8703	13706	1.57	3.0E-91	AF084530.1	NT	Homo sapiens cyclin-D binding Myo-like protein mRNA, complete cds
4458	9448	14429	6.17	3.0E-91	M30538.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4820	9804	14785	1.2	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4820	9804	14786	1.2	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C084
49	5130	10124	2.61	1.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1226	8225	11271	5.11	1.0E-91	AW449746.1	EST_HUMAN	U1-H-B13-eks-d-01-0-U1-s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2735280 3'
1222	6222	11265	7.33	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
1222	6222	11266	7.33	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
91	5168	10178	6.58	8.0E-92	W26387.1	EST_HUMAN	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA clone IMAGE:3614687 5'
283	5341	10354	7.99	8.0E-92	BE385363.1	EST_HUMAN	601273513f1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614687 5'
25	5105	10089	2.65	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
235	7716	10307	1	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
235	7716	10308	1	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
583	5817		0.83	7.0E-92	AF0078722.1	NT	Homo sapiens cytoplasmic Septinase truncated isoform mRNA, complete cds

Page 149 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1281	6269	11302	2.83	7.0E-92	4502364	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2123	7103	12216	8.39	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2123	7103	12216	8.39	7.0E-92	6031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2493	7461	12576	2.66	7.0E-92	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein 52 precursor, mRNA, complete cds
2853	7613	12723	5.83	7.0E-92	6005738	NT	Homo sapiens NRAS-related gene (D1S155E), mRNA
2879	7637	12762	0.93	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3270	10047	13304	0.87	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3270	10047	13305	0.87	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4455	9445	14425	1.24	7.0E-92	S11824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2880 nt]
4455	9445	14426	1.24	7.0E-92	S11824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2880 nt]
4844	8828	14801	0.84	7.0E-92	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
1652	6549		1.37	6.0E-92	BE390982.1	EST_HUMAN	601283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605018 5'
2692	7650	12764	2.21	3.0E-92	BE909714.1	EST_HUMAN	6011601242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3802839 5'
26	6106	10080	1.42	2.0E-92	4501688	NT	Homo sapiens acilin A receptor, type II (ACVR2B), mRNA
178	5241	10251	3.37	2.0E-92	11422846	NT	Homo sapiens hypothetical protein J446ZQ023.2 (DJ446ZQ023.2), mRNA
178	5241	10252	3.37	2.0E-92	11422846	NT	Homo sapiens hypothetical protein J446ZQ023.2 (DJ446ZQ023.2), mRNA
740	5763	10787	2.34	2.0E-92	BE298190.1	EST_HUMAN	601118237F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
740	6783	10788	2.34	2.0E-92	BE298190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1678	6672		1.45	2.0E-92	S78653.1	NT	mirg-mas-related (human, Genomic, 2416 nt)
1896	6884	11976	1.59	2.0E-92	AI8119.1	EST_HUMAN	wk27d07.X1 NC1 CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
1896	6884	11977	1.59	2.0E-92	AI8119.1	EST_HUMAN	wk27d07.X1 NC1 CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
1895	6879	12084	8.59	2.0E-92	4506860	NT	Homo sapiens syndecan 4 (syndecan, hyaluronan, proteoglycan, hydrolase) (SDC4) mRNA
2588	7551	12866	15.93	2.0E-92	6612457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2766	6611	11876	3.99	2.0E-92	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2766	6611	11877	3.99	2.0E-92	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
3632	8538	13543	1.16	2.0E-92	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
3532	8538	13544	1.16	2.0E-92	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3602	8509	13617	5.87	2.0E-92	5803180	NT	Homo sapiens stress-induced phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
4165	9180	14147	1.16	2.0E-92	M10876.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment

Page 150 of 209

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4835	9819		2.79	2.0E-92	AL040437.1	EST_HUMAN	DKFZp434C0414_r1_434 (synonym: ites3) Homo sapiens cDNA clone DKFZp434C0414 5'
1813	6803	11895	2.03	1.0E-92	R78078.1	EST_HUMAN	yl80e08_r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146574 5'
1813	6803	11896	2.03	1.0E-92	R78078.1	EST_HUMAN	yl80e08_r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146574 5'
2020	7003	12108	40.83	1.0E-92	45086689	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
1978	6984	12070	2.63	9.0E-93	AU1216B1.1	EST_HUMAN	AU1216B1 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
1891	6976		27.81	9.0E-93	AA316723.1	EST_HUMAN	EST18B114 HCC cell line (metastasis to liver in mouse) Homo sapiens cDNA 5' end similar to ribosomal protein L28
3534	8540	13546	1.76	9.0E-93	BE388571.1	EST_HUMAN	601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5'
4209	9202	14184	1.1	9.0E-93	AU1216B1.1	EST_HUMAN	AU1216B1 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
244	5304	10314	8.34	7.0E-93	AF231919.1	NT	Homo sapiens chromosome 21: unknown mRNA
1362	6359	11409	2.07	5.0E-93	AB014511.1	EST_HUMAN	Homo sapiens mRNA for KIAA0611 protein, partial cds
1383	6380	11429	8.53	5.0E-93	AJ674184.1	EST_HUMAN	wc08c08_x1 NCI CGAP_P28 Homo sapiens cDNA clone IMAGE:2314670 3'
1383	6380	11430	8.53	5.0E-93	AJ674184.1	EST_HUMAN	wc08c08_x1 NCI CGAP_P28 Homo sapiens cDNA clone IMAGE:2314670 3'
3162	8179	13200	4.58	5.0E-93	X0-201.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin
86	5163		5.69	4.0E-93	AA459833.1	EST_HUMAN	2x50e09_s1 Soares, testis_NIH Homo sapiens cDNA clone IMAGE:785888 3' similar to SW:CLPA_RAT
442	5479	10498	1.62	4.0E-93	4557879 NT	EST_HUMAN	P27397 CALPONIN_ACIDIC ISOFORM :
442	5479	10497	1.62	4.0E-93	4557879 NT	EST_HUMAN	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
783	5784	10812	4.03	4.0E-93	7657454 NT	EST_HUMAN	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
783	5784	10813	4.03	4.0E-93	7657454 NT	EST_HUMAN	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
1164	6167	11201	1.25	4.0E-93	8923858 NT	EST_HUMAN	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA
1932	6918	12017	3.59	4.0E-93	AFO47677.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
2183	7162	12282	0.93	4.0E-93	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
2533	7498	12618	1.01	4.0E-93	7656972 NT	EST_HUMAN	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
3487	8495	13512	0.79	4.0E-93	7705396 NT	EST_HUMAN	Homo sapiens tumor antigen SLP-8p (HCCB), mRNA
3935	8934	13927	6.14	4.0E-93	4604654 NT	EST_HUMAN	Homo sapiens interleukin 18 receptor 1 (IL18R1) mRNA
4883	8495	13512	0.83	4.0E-93	7705396 NT	EST_HUMAN	Homo sapiens tumor antigen SLP-8p (HCCB), mRNA
3567	8574	13579	19.66	3.0E-93	BF989030.1	EST_HUMAN	602246554F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4332038 5'
3567	8574	13580	19.66	3.0E-93	BF989030.1	EST_HUMAN	602246554F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4332038 5'
180	6254	10285	3.68	2.0E-93	AB016610.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
190	5254	10286	3.68	2.0E-93	AB015610.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
321	5376	10386	8.39	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
322	6376	10386	8.39	2.0E-93	AL163286.2	NT	Homo sapiens chromosome 21 segment HS21C085
2072	7054	12184	1.86	2.0E-93	U40763.1	NT	Human Cik-associated RS cyclophilin CAR5-Cyp mRNA, complete cds

Page 151 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2416	7387	12507	1.74	2.0E-93	BE262982.1	EST_HUMAN	601117586F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3358220 5'
4966	8943	14920	1.01	2.0E-93	BE263201.1	EST_HUMAN	601116810F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357243 5'
102	5179	10189	2.66	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
102	6179	10180	2.66	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
514	6549	10554	1.748	1.0E-93	7857016	NT	Homo sapiens hypothetical protein (D328E19.G1.1), mRNA
695	5626	10625	3.87	1.0E-93	AI146755.1	EST_HUMAN	094608.x1 NC1_CGAP CLL1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q62384 Q62384
861	5880	10821	7.39	1.0E-93	DB7675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1217	6216	11256	8.15	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20281), mRNA
1217	6216	11257	8.15	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20281), mRNA
1325	6323	11370	1.13	1.0E-93	AB046783.1	NT	Homo sapiens mRNA for KIAA1533 protein, partial cds
1327	6325	11372	3.03	1.0E-93	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2276	7252	12370	6.14	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2394	7385	12487	12.91	1.0E-93	AF055086.1	NT	Homo sapiens MHC class 1 region
2435	7406	131	1.31	1.0E-93	AL137200.1	NT	Novel human gene mapping to chromosome 1
2749	8276	11316	1.39	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532865 5'
2749	8276	11316	1.39	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532865 5'
2883	7883	12803	3.34	1.0E-93	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
3144	8160		1.76	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4305	9297	14283	2.36	1.0E-93	AL163284.2	NT	Homo sapiens chromosome 21 segment HS2C1084
3856	8958	13864	3.44	6.0E-94	AF142482.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
1805	8797		36.53	4.0E-94	LO5694.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2586	7549	12664	1.13	4.0E-94	46086008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PP1R10) mRNA
3587	8594	13598	1.02	4.0E-94	AW197851.1	EST_HUMAN	xr889f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
3587	8594	13599	1.02	4.0E-94	AW197851.1	EST_HUMAN	xr889f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
4578	8567	14556	3.55	4.0E-94	AI691312.1	EST_HUMAN	PROTEIN TYROSINE PHOSPHATASE ;
607	9634	10835	3.13	3.0E-94	AB0227785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to <i>Drosophila</i> <i>ash2</i> gene
711	6735	10751	1.52	3.0E-94	4502806	NT	Homo sapiens complement component 5 (C5) mRNA
1701	6696	11772	3.56	3.0E-94	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1701	6696	11773	3.56	3.0E-94	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1735	6730	11807	6.42	3.0E-94	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA

Table 4
Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4065	8059	14046	0.67	3.0E-94	AA164805.1	EST_HUMAN	2v63g08.11 Scares_fetal_fetus_Nr2Hf8_Sw_Homo_sapiens cDNA clone IMAGE:774782 5'
5051	10022	14691	0.7	3.0E-94	4507848	NT	Homo sapiens ubiquitin specific protease 13 (Isopeptidase T-3) (USP13) mRNA
148	5214	10228	2.88	1.0E-94	BE285714.1	EST_HUMAN	601175762F1NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3015	8032	13042	2.59	1.0E-94	BE253433.1	EST_HUMAN	601111686F1NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3015	8032	13043	2.59	1.0E-94	BE253433.1	EST_HUMAN	601111686F1NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
4233	8227	14211	1.7	1.0E-94	95068692	NT	Homo sapiens hypothetical protein (FLJ20748) mRNA
1447	6444	11503	5.95	9.0E-95	AF027302.1	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3082	8098	13112	1.09	9.0E-95	7662021	NT	Homo sapiens KIAA0255 gene product (KIAA0255) mRNA
3082	8098	13113	1.09	9.0E-95	7662021	NT	Homo sapiens KIAA0255 gene product (KIAA0255) mRNA
							ve09e04_x1_NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340608 3' similar to gb:K00558
4406	8397	14380	3.37	8.0E-95	AI700988.1	EST_HUMAN	TUBULIN ALPH-1 CHAIN (HUMAN);
4406	8397	14381	3.37	8.0E-95	AI700988.1	EST_HUMAN	ve09e04_x1_NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340608 3' similar to gb:K00558
273	5332	10344	10.63	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
273	5332	10345	10.63	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4241	9235	14219	5.66	7.0E-95	MB8708.1	NT	Homo sapiens Ly-6-like protein (CD59) mRNA, complete cds
4289	9281		1.4	7.0E-95	AI_163246.2	NT	Homo sapiens chromosome 21 segment HS21CO46
1605	6601	11662	3.13	2.0E-95		7662021	Homo sapiens KIAA0255 gene product (KIAA0255) mRNA
1605	6601	11863	3.13	2.0E-95		7662021	Homo sapiens KIAA0255 gene product (KIAA0255) mRNA
1801	6888	11982	3.11	2.0E-95	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorby fundus dystrophy, pseudodinflammatory) (TIMP3) mRNA
1804	6891	11988	1.74	2.0E-95	BE393873.1	EST_HUMAN	601312161F1NIH_MGC_44 Homo sapiens cDNA clone IMAGE:36588862 5'
2359	7333	12449	1.55	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2359	7333	12450	1.65	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2396	7367	12468	2.79	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2442	7412	12628	1.84	2.0E-95	4758423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl) carrier (GCSH) mRNA
3084	8100	13115	1.85	2.0E-95	AF015452.1	NT	Homo sapiens Ursulin-gamma mRNA, complete cds
3484	8492	13508	2.78	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168) mRNA
3484	8492	13509	2.78	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168) mRNA
3537	8543	13549	1.17	2.0E-95	AB037607.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
3684	8669	13874	1	2.0E-95	AI280284.1	EST_HUMAN	qm01c02_x1_Scares_NiHMPu_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP:T23G7.4 CE03705;
4236	9230	14213	1.61	2.0E-95	7657165	NT	Homo sapiens hypothetical protein (HS322B1A) mRNA

Page 153 of 209

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4873	8852	14827	2.65	2.0E-95	7661978	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4917	8895	14869	0.92	2.0E-95	AA147831.1	EST_HUMAN	2x11d07.11 Soares_fetal_fetus_Nb2HF8_5w Homo sapiens cDNA clone IMAGE:788157_6'
4917	8895	14870	0.92	2.0E-95	AA147831.1	EST_HUMAN	2x11d07.11 Soares_fetal_fetus_Nb2HF8_5w Homo sapiens cDNA clone IMAGE:788157_5'
439	7720	10493	3.42	8.0E-98	BE07607.1	EST_HUMAN	601487608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898761_5'
439	7720	10494	3.42	8.0E-98	BE07607.1	EST_HUMAN	601487608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898761_5'
3813	8816	13822	1.18	7.0E-86	AF231820.1	NT	Homo sapiens chromosome 21 unknown mRNA
2168	7176	12289	2.4	6.0E-86	BE171984.1	EST_HUMAN	MR0-HT0559-285200-002-d07 HT0559 Homo sapiens cDNA
3244	8257	13278	0.86	6.0E-86	AL1632012	NT	Homo sapiens chromosome 21 segment HS21C001
3402	8411	13437	3.71	6.0E-98	M26973.1	NT	Human Glyceraldehyde-3-phosphate dehydrogenase pseudogene 3' end
318	5373	10382	3.23	5.0E-96	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
832	5851	10889	3.33	5.0E-96	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
832	5851	10890	3.33	5.0E-96	AB032988.1	NT	Homo sapiens mRNA for phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2545	7510		2.15	5.0E-96	11416767	NT	Homo sapiens DNA for monoamine oxidase type A (7) (partial)
4748	9733		1.28	5.0E-96	X80812.1	NT	Homo sapiens DNA for monoamine oxidase type A (7) (partial)
4087	9061		10.35	5.0E-96	H688656.1	EST_HUMAN	Y87h12.11 Soares_fetal_liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:212927_5'
412	6449		4.94	2.0E-98	4603098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
738	5761	10784	1.2	2.0E-98	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C04B
738	6749	11832	1.81	2.0E-98	7706205	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA
4613	8589	14855	2.68	2.0E-98	BE148074.1	EST_HUMAN	RC3-HT0230-040500-110-902 HT0230 Homo sapiens cDNA
663	6689	10698	2.97	1.0E-96	Y18880.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1743	6738	11814	4.56	1.0E-96	AW855054.1	EST_HUMAN	EST367124 IMAGE resequences, MAGC Homo sapiens cDNA
1743	6738	11815	4.68	1.0E-96	AW855054.1	EST_HUMAN	EST367124 IMAGE resequences, MAGC Homo sapiens cDNA
2204	7705	12305	1.95	1.0E-96	US1472.2	NT	Felis catus superfast myosin heavy chain (sMHC) mRNA, complete cds
925	6942	10976	3.84	4.0E-97	BE044436.1	EST_HUMAN	QH0-BN0106-170300-293-a06 BN0106 Homo sapiens cDNA
1867	6856	11944	1.34	4.0E-97	5453572	NT	Homo sapiens briefdin A-Inhibited guanine nucleotide-exchange protein 2 (BIP2), mRNA
241	5302	10312	2.28	3.0E-97	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
883	5882	10923	9.5	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
883	5882	10924	9.5	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1415	7747	11473	1.64	3.0E-97	4756813	NT	Homo sapiens N-myc (end STAT) Interactor (NMI), mRNA
2371	7706	12462	2.86	3.0E-97	U36255.1	NT	Human beta-prime-adaplin (BAM22) gene, exon 7
3186	6202	13224	1.14	3.0E-97	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
4635	6820	14612	35.24	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA

Page 154 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
890	8508	10848	6.71	9.0E-98	BE080973.1	EST_HUMAN	PMA4_BT0724-010400-008-a12_BT0724_Homo sapiens cDNA
1257	6225	11287	1.1	9.0E-98	85930092.NT		Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
6021	8982	14966	1.03	9.0E-98	11416594.NT		Homo sapiens FSH primary response (LRRP1, rat) homolog 1 (FSHFRH1), mRNA
24	5104		4.32	8.0E-98	A1251158.1	NT	Homo sapiens partial MICB gene for MHC class I chain-related protein B, exons 2-3 and joined CDS
1529	8526	11564	1.06	8.0E-98	5031810.NT		Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1529	6528	11565	1.06	8.0E-98	5031810.NT		Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1688	6884	11758	3.31	8.0E-98	AB017007.1	NT	Homo sapiens PM2SL18 mRNA, partial cds
1688	6684	11750	3.31	8.0E-98	AB017007.1	NT	Homo sapiens PM2SL18 mRNA, partial cds
3706	8710	13713	6.04	8.0E-98	104469.1	NT	Human mitochondrial creatine kinase (CKM1) gene, complete cds
2113	7099	12207	1.06	3.0E-98	A1403124.1	EST_HUMAN	AJ403124.3 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
2534	7499	12618	1.4	3.0E-98	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2876	7634	2.13	3.0E-98	AA077498.1	EST_HUMAN	7B18H101 Chromosome 7 fetal brain cDNA library Homo sapiens cDNA clone 7B18H01	
726	5748	10770	2.43	2.0E-98	BE261684.1	EST_HUMAN	601149486F1 NIH_MGC_19_Homo sapiens cDNA clone IMAGE:3620245 5'
2028	7009	12115	2.25	2.0E-98	BE284281.1	EST_HUMAN	601172858F1 NIH_MGC_17_Homo sapiens cDNA clone IMAGE:3628134 5'
2178	7165	12275	2.4	2.0E-98	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
3988	8987	13973	0.94	2.0E-98	8923308.NT		Homo sapiens hypothetical protein FLJ20333 (FLJ20333), mRNA
4172	9167	14154	0.68	2.0E-98	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4214	E207	14186	3.27	2.0E-98	4756331.NT		Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4680	9685	14846	1.61	2.0E-98	AF2118902.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 16
4680	9865	14847	1.61	2.0E-98	AF2118902.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 16
403	5439	10459	91.85	1.0E-98	AI862007.1	EST_HUMAN	W36004.X1 NC1 CGAP_J11 Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW.RL2B_HUMAN
452	5489	10504	2.47	1.0E-98	AW098611.1	EST_HUMAN	P28316.805 RIBOSOMAL PROTEIN L23A.
1761	8753	111838	68.95	1.0E-98	N48818.1	EST_HUMAN	PIM0-BN0065-100300-001-c08 BN0065_Homo sapiens cDNA
2069	7051	12159	1.5	6.0E-99	11430555.NT		Y723105.11 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2435885 6' similar to
2069	7051	12160	1.5	6.0E-99	11430555.NT		Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
4605	9593	14579	1.1	6.0E-99	4502680.NT		Homo sapiens CD34 antigen (CD34) mRNA
1924	6910	12006	0.92	5.0E-99	Y11385.1.NT		H1_sapiens IMPA gene, exon 8
4432	8422	14408	1.25	5.0E-99	AF009860.1.NT		Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
4586	8574	14564	1.82	5.0E-99	AF265555.1.NT		Homo sapiens ubiquitin-conjugating B1R-domain enzyme APOLLON mRNA, complete cds
4586	9574	14565	1.82	5.0E-99	AF265555.1.NT		Homo sapiens ubiquitin-conjugating B1R-domain enzyme APOLLON mRNA, complete cds

Page 155 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Transcript
1220	8220		21.29	2.0E-99	AW274792.1	EST_HUMAN	xp09606_x1 NCI CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN LIGHT CHAIN ALKALI_NON MUSCLE ISOFORM (HUMAN);
3184	8220	13223	2.08	2.0E-99	M30838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4412	8402	14387	2.65	2.0E-99	AF095103.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
313	5368	10379	1.21	1.0E-99	AF114497.1	NT	Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds
378	5425	10440	1.23	1.0E-99	11526160	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
1398	6393	11447	8.91	1.0E-99	M30838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1525	6522	11579	3.27	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1525	6522	11579	3.27	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1886	6875	11884	1.12	1.0E-99	4803730	NT	Homo sapiens FK506-binding protein 6 (38kD) (FKBP6) mRNA, and translated products
1886	6875	11885	1.12	1.0E-99	4803730	NT	Homo sapiens FK506-binding protein 6 (38kD) (FKBP6) mRNA, and translated products
3011	80228	13039	1.27	1.0E-99	JO3171.1	NT	Human Interferon-alpha receptor (HuIFN-alpha-Reo) mRNA, complete cds
4255	9249	14233	2.45	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4255	9249	14234	2.45	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
1	5083	10087	1.68	1.0E-99	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2	5083	10087	1.64	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
67	6146	10161	1.24	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related Protein on Y (XKRY), mRNA
67	5146	10152	1.24	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related Protein on Y (XKRY), mRNA
85	5162	10174	2.54	1.0E-100	AW275237.1	EST_HUMAN	x78b11.1 NCI CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2824605 3'
168	5233	10243	0.69	1.0E-100	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
315	5370	10381	1.05	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
341	5393	10400	1.8	1.0E-100	T05087.1	EST_HUMAN	EST02975 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCR32
434	5472		1.98	1.0E-100	AF003528.1	NT	Homo sapiens X-linked arthritidic ectodermal dysplasia protein gene (EDA), exon 2 and 1 ranking repeat regions
486	6523		19.01	1.0E-100	X89631.1	NT	Gorilla DNA for ZNF80 gene homolog
506	6541	10547	1.38	1.0E-100	BE180009.1	EST_HUMAN	RC3-H10625-040500-022-b09 H10625 Homo sapiens cDNA
1003	6013	11042	2.48	1.0E-100	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1003	6013	11043	2.48	1.0E-100	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1614	6512		1.64	1.0E-100	AW207655.1	EST_HUMAN	U-H-B1-8f-c-07-0-U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
1519	6516	11573	1.15	1.0E-100	AI200857.1	EST_HUMAN	q6209.x1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1764633 3' similar to SW:CYT_COT1A
1827	6817	11911	1.44	1.0E-100	AB032894.1	NT	P81061 CYSTATIN :
2634	7594	12707	1.62	1.0E-100	11418976	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds

Page 156 of 209

Table 4
Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2852	7071			4.16 1.0E-100	D1078.1 NT		<i>Homo sapiens RGH2 gene, retrovirus-like element</i>
4089	9083	14074		1.57 1.0E-100	AF057354.1 NT		<i>Homo sapiens myotubularin-related protein 1a mRNA, partial cds</i>
4114	9108	14083		2.28 1.0E-100	4503792 NT		<i>Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA</i>
4920	8988	14872		3.82 1.0E-100	6032104 NT		<i>Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA</i>
4920	8998	14873		3.82 1.0E-100	6032104 NT		<i>Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA</i>
76	5154	10164		1.88 1.0E-101	7110714 NT		<i>Homo sapiens SEC14 (S. cerevisiae) like 2 (SEC14L2) mRNA</i>
76	6164	10165		1.88 1.0E-101	7110714 NT		<i>Homo sapiens SEC14 (S. cerevisiae) like 2 (SEC14L2) mRNA</i>
877	5702	10710		2.59 1.0E-101	AB007915.2 NT		<i>Homo sapiens mRNA for KIA0446 protein, partial cds</i>
694	5718	10735		6.32 1.0E-101	7110734 NT		<i>Homo sapiens ventral anterior homeobox 2 (VAX2) mRNA</i>
694	5718	10736		6.32 1.0E-101	7110734 NT		<i>Homo sapiens ventral anterior homeobox 2 (VAX2) mRNA</i>
762	5783	10811		4.84 1.0E-101	7657454 NT		<i>Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1) mRNA</i>
843	5862	10902		3.85 1.0E-101	4503914 NT		<i>Homo sapiens phosphotribosemicarnamide formyltransferase, phosphotribosemicarnamide synthetase (GART) mRNA</i>
970	5985	11020		34.36 1.0E-101	BF681228.1 EST HUMAN		<i>Homo sapiens cDNA clone IMAGE:4297281 5'</i>
1035	6045	11074		1.9 1.0E-101	A122187.1 EST HUMAN		<i>NFL-1 GBC-51 Homo sapiens cDNA clone IMAGE:1843336 3'</i>
1548	6546	11608		2.07 1.0E-101	5921460 NT		<i>Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA</i>
1548	6546	11607		2.07 1.0E-101	5921460 NT		<i>Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA</i>
1707	6702	11779		1 1.0E-101	76621183 NT		<i>Homo sapiens KIAA0569 gene product (KIAA0569), mRNA</i>
1707	6702	11780		1 1.0E-101	76621183 NT		<i>Homo sapiens KIAA0569 gene product (KIAA0569), mRNA</i>
1805	6892	11987		1.32 1.0E-101	4502996 NT		<i>Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1) mRNA</i>
2003	6986	12080		2.61 1.0E-101	BE843070.1 EST HUMAN		<i>RC3-S10281-160600-016-h09 ST0281 Homo sapiens cDNA</i>
2288	7767	12381		0.97 1.0E-101	5728862 NT		<i>Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA</i>
2541	7505	12825		6.73 1.0E-101	X72893.1 NT		<i>H. sapiens EW gene, exon 5</i>
2870	7628	12741		5.15 1.0E-101	AJ237744.1 NT		<i>Homo sapiens RIBIR gene (partial), exon 12</i>
2870	7628	12742		5.15 1.0E-101	AJ237744.1 NT		<i>Homo sapiens RIBIR gene (partial), exon 12</i>
2884	7803			12.51 1.0E-101	AJ262312.1 NT		<i>Homo sapiens genomic downstream Rhesus box</i>
3130	8146	13167		2.4 1.0E-101	48865270 NT		<i>Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA</i>
3167	8183			2.76 1.0E-101	BF035327.1 EST HUMAN		<i>601488531F1 NIH MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'</i>
3298	8307	13332		2.01 1.0E-101	AW86556.1 EST HUMAN		<i>EST377629 MAGE resequences, MAGI Homo sapiens cDNA</i>
3310	7628	12741		3.42 1.0E-101	AJ237744.1 NT		<i>Homo sapiens RIBIR gene (partial), exon 12</i>
3310	7628	12742		3.42 1.0E-101	AJ237744.1 NT		<i>Homo sapiens RIBIR gene (partial), exon 12</i>
3175	8788	13782		5.05 1.0E-101	AB022705.1 NT		<i>Homo sapiens ASH2L gene, complete cds, similar to <i>Drosophila ash2</i> gene</i>
4868	9847	14823		1.61 1.0E-101	6921460 NT		<i>Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA</i>
4868	9847	14824		1.61 1.0E-101	6921460 NT		<i>Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA</i>

Page 157 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
40	5120	10103	0.98	1.0E-102	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (PLAK230) mRNA, complete cds
339	5391	10397	4.65	1.0E-102	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
615	5642	10845	0.83	1.0E-102	BE262470.1	EST_HUMAN	601108282F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5'
768	5787	10816	0.81	1.0E-102	46575334	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1100	6107	11137	3.79	1.0E-102	MI10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1249	6247	11287	1.82	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1249	6247	11288	1.82	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1384	6391	11444	373.13	1.0E-102	BE40847.1	EST_HUMAN	601289962F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629901 5'
2248	7223	12342	3.39	1.0E-102	AI124668.1	EST_HUMAN	am60c10_x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538954 3' similar to SW:GG95_HUMAN Q08379_GOLGIN-85.
2248	7223	12343	3.39	1.0E-102	AI124668.1	EST_HUMAN	am60c10_x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538954 3' similar to SW:GG95_HUMAN Q08379_GOLGIN-85.
2786	7807	12824	0.69	1.0E-102	11418442	NT	Homo sapiens peroxisome biogenesis factor 1 (PEX1), mRNA
2991	8009	13022	1.4	1.0E-102	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
3060	8077	13089	2.88	1.0E-102	AU141005	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
3060	8077	13090	2.88	1.0E-102	AU141005	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4111	9105	14081	1.63	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C1007
4287	9279	14267	2.09	1.0E-102	BE251310.1	EST_HUMAN	601107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:334382 5'
4948	9925	14803	1.17	1.0E-102	R6648.1	EST_HUMAN	6011500405F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:140934 5'
68	6147	10163	1.86	1.0E-103	BE9081158.1	EST_HUMAN	6011500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3802305 5'
68	6147	10154	1.86	1.0E-103	BE9081158.1	EST_HUMAN	6011500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3802305 5'
99	6176	10186	7.11	1.0E-103	D87078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
208	5272	10284	9	1.0E-103	5453793	NT	Homo sapiens nucleolar protein (KED repeat) (NOP56) mRNA
966	6591	11013	0.87	1.0E-103	AJ278348.1	NT	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPP-E gene)
1224	6323	11269	8.76	1.0E-103	BE877541.1	EST_HUMAN	601485388F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:388178 5'
1581	6658	11620	3.06	1.0E-103	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (PLAK230) mRNA, complete cds
1870	6659	11947	0.99	1.0E-103	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SNAP), mRNA
1830	6916	12013	1.28	1.0E-103	4502428	NT	Homo sapiens bone morphogenic protein 8 (osteogenic protein 2) (BMP8) mRNA
1830	6916	12014	1.28	1.0E-103	4602428	NT	Homo sapiens bone morphogenic protein 8 (osteogenic protein 2) (BMP8) mRNA
2242	7219	12338	2.16	1.0E-103	AU1134991.1	EST_HUMAN	AU1134991 PLACE0009865 5'
2383	7354	12476	1.58	1.0E-103	AF060568.1	NT	Homo sapiens primate-specific leukaemia zinc finger protein (PLZF) gene, complete cds
2547	7512	12630	1.26	1.0E-103	NS2770.1	EST_HUMAN	W491d08.91 Soares, placenta, 8loc9weeks, 2NbHP81c9W Homo sapiens cDNA clone IMAGE:259599 3'
2895	8013	2.58	1.0E-103	BE744722.1	EST_HUMAN	601573113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3334316 5'	

Page 158 of 209
 Table 4 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal No:	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							Top Hit Descriptor	Top Hit Descriptor
3295	8306	13331	4.02	1.0E-103	AW288245.1	EST_HUMAN	U1-H-BW0-ell-h-11-0-U1_s1 INCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:2733165 3'	
3395	8363	13379	1.23	1.0E-103	AB046892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds	
3669	8674		9	1.0E-103	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds	
3704	8708	13711	1.2	1.0E-103	AA485663.1	EST_HUMAN	ab10d12_s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element;	
3759	8743	13743	1.26	1.0E-103	11430076	NT	Homo sapiens neuropilin 1 (NRIP1), mRNA	
3897	8897	13895	2.44	1.0E-103	T23883.1	EST_HUMAN	seq340 b4HB3MA-Cot109+4-10-Bio Homo sapiens cDNA clone b4HB3MA-Cot108+10-Bio-7 3'	
4646	9631	14626	3.54	1.0E-103	AL1632278.2	NT	Homo sapiens chromosome 21 segment HS21/C078	
233	5296	12905	4.73	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1_564 (synonym: hib2) Homo sapiens cDNA clone DKFZp564H1072 5'	
233	6296	10306	4.73	1.0E-104	AL037548.3	EST_HUMAN	DKFZp564H1072_r1_564 (synonym: hib2) Homo sapiens cDNA clone DKFZp564H1072 6'	
1849	6638	11827	1.83	1.0E-104	4802428	NT	Homo sapiens bone morphogenic protein 8 (osteogenic protein 2) (BMP8) mRNA	
2131	7111	12224	5.4	1.0E-104	AA132876.1	EST_HUMAN	zg22c06_s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:587626 3' similar to	
2141	7120	12236	6.85	1.0E-104	BB744828.1	EST_HUMAN	gb:Z14116 Homo sapiens CD1 ma1 CD56 Glycoprotein PRECURSOR (HUMAN);	
2308	7283	12402	3.55	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110800-21-4-12 CT0249 Homo sapiens cDNA	
2308	7283	12403	3.55	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110800-21-4-12 CT0249 Homo sapiens cDNA	
2370	7343	12461	6.02	1.0E-104	5031570	NT	Homo sapiens ARF2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA	
2430	7401	12519	1.36	1.0E-104	7682126	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA	
2430	7401	12520	1.36	1.0E-104	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA	
2800	7820	12837	6.92	1.0E-104	M34671.1	NT	Human lymphocytic antigen CD59(MEM43 mRNA, complete cds	
2846	7868		2.57	1.0E-104	Y11151.1	NT	H.sapiens gene encoding phenylpyruvate lautomerase II	
3189	8205	13227	0.85	1.0E-104	AU132926.1	EST_HUMAN	AU130926_QVARC1 Homo sapiens cDNA clone QVARC1:0000836 5'	
3307	8318		1.84	1.0E-104	AU1319436.1	EST_HUMAN	EST:21658 Adrenal gland tumor Homo sapiens cDNA 5' end	
3839	8841	13848	1.14	1.0E-104	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds	
4008	9004	13982	1.24	1.0E-104	F11745.1	EST_HUMAN	HSC31A071 normalized infant brain cDNA Homo sapiens cDNA clone c-318d7	
4252	9248	14230	4.98	1.0E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)	
4477	9467	14446	1.5	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA	
4477	9467	14447	1.5	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA	
276	7691	10348	3.85	1.0E-105	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-1), Alzheimer disease) (APP), mRNA	
422	5080	10084	19.42	1.0E-105	4505160	NT	Homo sapiens Mais1 (mouse) homolog (MEIS1) mRNA	
589	5820	10818	6.63	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds	
589	5620	10619	6.63	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds	
1840	6837		5.48	1.0E-105	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds	

Page 159 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1667	6663	11738		1.04	1.0E-105 AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1785	6777	11859		1.78	1.0E-105 AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1885	6874	11863		1.62	1.0E-105 D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds
2128	7105	12220		5.92	1.0E-105 AA318589.1	EST_HUMAN	EST20609 Spleen 1 Homo sapiens cDNA 5' end similar to autoimmune antigen Ku, p70/p80 subunit
2260	7237			1.56	1.0E-105 BEE91168.1	EST_HUMAN	60143491F_NIH_MGC_72 Homo sapiens cDNA clone IMAGE:391B511 5'
2849	7609			0.96	1.0E-105 AA584408.1	EST_HUMAN	no10d05.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:110265 3'
2837	7856			3.39	1.0E-105 A1229041.1	NT	Homo sapiens B59 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
3252	8265	13286		1.32	1.0E-105 Bf347753.1	EST_HUMAN	602022695F_NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158143 5'
3252	8265	13287		1.32	1.0E-105 Bf347753.1	EST_HUMAN	602022695F_NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158143 5'
3981	8979	13984		6.06	1.0E-105 AW9816088.1	EST_HUMAN	EST313761 IMAGE sequences, MACSG Homo sapiens cDNA
4781	9765			4.42	1.0E-105 AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
4934	9911	14889		0.92	1.0E-105 AB018339.1	NT	Homo sapiens mRNA for KIAA0786 protein, partial cds
4974	9950	14928		1.08	1.0E-105 AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
4987	9861	14938		0.87	1.0E-105 AW86616.1	EST_HUMAN	EST378088 IMAGE sequences, MAGI Homo sapiens cDNA
159	5246			1.69	1.0E-108 AW503208.1	EST_HUMAN	U1-HF-BNG-akr-9-07-0-U1 NIH_MAC_50 Homo sapiens cDNA clone IMAGE:3078348 6'
205	6269	10282		2.72	1.0E-108 AI565055.1	EST_HUMAN	1a79c01.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2215008 3'
637	6572	10576		1.81	1.0E-108 AW985658.1	EST_HUMAN	EST377639 IMAGE sequences, MAGI Homo sapiens cDNA
602	6581	10531		8.07	1.0E-108 J00146.1	NT	Human dihydrofolate reductase pseudogene (psi-hd1)
603	6531	10651		6.16	1.0E-108 J00146.1	NT	Human dihydrofolate reductase pseudogene (psi-hd1)
1492	6490	11845		1.76	1.0E-108 AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
1662	66538	11732		3.2	1.0E-108 U48724.1	NT	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1681	6877	11751		2.79	1.0E-108 U04510.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 41
1767	6759	11845		3.22	1.0E-108 AA527446.1	EST_HUMAN	ng1c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element.
1767	6759	11846		3.22	1.0E-108 AA527446.1	EST_HUMAN	ng1c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element.
2063	7045	12153		1.25	1.0E-108 BE144286.1	EST_HUMAN	MRO-HT0165.1-140200-008-d110 HT0165 Homo sapiens cDNA
2253	7230	12349		10.26	1.0E-108	4504184 NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2432	7403	:	12522	1.47	1.0E-108 AF000528.1	NT	Homo sapiens X-linked amniotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2525	7491	12611		1	1.0E-108 U64675.2	NT	Homo sapiens sperm membrane protein BS-63 mRNA, complete cds
2527	7493	12613		1.49	1.0E-108 BE260201.1	EST_HUMAN	60149783F_NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3602461 5'
2683	7641	12557		10	1.0E-108 AI276526.1	EST_HUMAN	q76h10.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:11878307 3'
2752	8404	11462		7.19	1.0E-106	4504184 NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA

Page 160 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2752	6404	11463	7.19	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2805	7825	12840	1.79	1.0E-108	BE384288.1	EST_HUMAN	60122675F1 NIH MGC_20 Homo sapiens cDNA clone IMAGE:3613818 5'
2870	7889	12910	4.45	1.0E-108	AB0317747.1	NT	Homo sapiens mRNA for KIAA1328 protein, partial cds
2870	7889	12911	4.45	1.0E-108	AB0317747.1	NT	Homo sapiens mRNA for KIAA1328 protein, partial cds
3107	8123	13141	2.41	1.0E-108	89228865	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3107	8123	13142	2.41	1.0E-108	8922885	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3356	8364	13280	0.99	1.0E-108	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3356	8364	13281	0.99	1.0E-108	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3714	8718	13719	0.92	1.0E-108	AF001445.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 2
3926	8926	13916	10.11	1.0E-108	AW974690.1	EST_HUMAN	EST386875 MAGE resequences, MAGN Homo sapiens cDNA
3926	8926	13917	10.11	1.0E-108	AW974690.1	EST_HUMAN	EST386875 MAGE resequences, MAGN Homo sapiens cDNA
3844	8942	13932	1.74	1.0E-108	5729729	NT	Homo sapiens API5-like 1 (AP15L1), mRNA
4470	9460	14439	0.67	1.0E-108	BE144286.1	EST_HUMAN	MRO-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
4741	9726	14711	1.39	1.0E-108	U31520.1	NT	Human alphamannosidase II mRNA, complete cds
234	6297		3.3	1.0E-107	AJ271735.1	NT	Human sapiens Xq pseudautosomal region, segment 17/2
282	5321		1.47	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
624	6651	10655	2.22	1.0E-107	AF155103.1	NT	Human sapiens NY-REN-25 antigen mRNA, partial cds
803	5824	10854	1.94	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
875	5893	10834	1.25	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
954	6970	11003	8.1	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1259	6257	11300	2.22	1.0E-107	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1536	6534	11593	8.86	1.0E-107	BF087405.1	EST_HUMAN	QV2-HT0540-120900-358-e05 HT0540 Homo sapiens cDNA
1713	6708	11784	4.61	1.0E-107	AF136275.1	NT	Homo sapiens cathepsin Z precursor (CTSZ) gene, exon 3
1804	6795	11885	2.87	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1804	6795	11886	2.87	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2146	7125	12242	1.06	1.0E-107	U13129.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2301	7276	12395	4.22	1.0E-107	AW842451.1	EST_HUMAN	PMI-CN0031-180100-001-d03 CN0031 Homo sapiens cDNA
2301	7276	12396	4.22	1.0E-107	AW842451.1	EST_HUMAN	PMI-CN0031-180100-001-d03 CN0031 Homo sapiens cDNA
2463	7432	12650	1.65	1.0E-107	BE732480.1	EST_HUMAN	6011567619F1 NIH MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2463	7432	12651	1.65	1.0E-107	BE732460.1	EST_HUMAN	6011567619F1 NIH MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2938	7957	12874	3.71	1.0E-107	AW842451.1	EST_HUMAN	PMI-CN0031-180100-001-d03 CN0031 Homo sapiens cDNA
2938	7957	12975	3.71	1.0E-107	AW842451.1	EST_HUMAN	PMI-CN0031-180100-001-d03 CN0031 Homo sapiens cDNA
3026	8043	13052	7.53	1.0E-107	5902097	NT	Homo sapiens SMT3 (suppressor of mRNA 3, yeast) homolog 2 (SM3H2), mRNA

Page 161 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3736	8740	13739	5.33	1.0E-107	AF020671.1	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
940	5957	10990	2.88	1.0E-108	BE286042.1	EST_HUMAN	601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
1246	6244	11284	6.83	1.0E-108	Y18000.1	NT	Homo sapiens NF2 gene
2025	7008	12114	1.65	1.0E-108	BF026128.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3854938 5'
							bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2883899 3' similar to gb:X537776 60S RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);
2380	7334	12451	12.25	1.0E-108	BE206694.1	EST_HUMAN	h12811.x1 NCI CGAP_G11 Homo sapiens cDNA clone IMAGE:2872060 3' similar to SW:3BP1_MOUSE P65184 SH3-BINDING PROTEIN 3BP-1.
4033	9029	14017	1.15	1.0E-108	AW664438.1	EST_HUMAN	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4394	9385	14387	3.04	1.0E-108	U72981.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4394	9385	14388	3.04	1.0E-108	U72981.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4659	8844	14632	3.68	1.0E-108	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4765	9749	14737	0.88	1.0E-108	AW504789.1	EST_HUMAN	U1-HF-BN0-ah-e-04-U1 r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:30801988 5'
4791	9775	14759	2.91	1.0E-108	AJ008005.1	NT	Homo sapiens PSNI gene, alternative transcript
4962	8939	14918	0.95	1.0E-108	6031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
4988	9982	14939	0.72	1.0E-108	Y12490.1	NT	Homo sapiens mRNAs for Golgi-associated microtubule-binding protein (GMAP-210)
43	6123	10111	2.46	1.0E-109	AW803116.1	EST_HUMAN	IL2-JM0077-260400-079-D0077 Homo sapiens cDNA
66	5145	10150	3.94	1.0E-109	D86974.1	NT	Human mRNA for KIAA0220 gene, partial cds
218	5281	10282	0.76	1.0E-109	11422488	NT	Human sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
226	5288	10298	7.69	1.0E-109	11428391	NT	Human sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
484	6601	10511	8.2	1.0E-109	4507712	NT	Human sapiens leucine-rich repeat domain 2 (TTC2) mRNA
593	6624	10623	15.28	1.0E-109	AB023216.1	NT	Human sapiens mRNA for KIAA0996 protein, partial cds
593	5624	10624	15.28	1.0E-109	AB023216.1	NT	Human sapiens mRNA for KIAA0996 protein, partial cds
1183	6185	11222	93.77	1.0E-109	M2889.1	NT	Human sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1184	6185	11222	72.21	1.0E-109	M2889.1	NT	Human sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1510	6508	11564	1.52	1.0E-109	BE283673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859838 6'
1510	6508	11565	1.52	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859838 6'
1836	6826	11914	5.54	1.0E-109	D13643.2	NT	Human sapiens mRNA for KIAA0018 protein, partial cds
2181	7180	12280	2.32	1.0E-109	AL163284.2	NT	Human sapiens chromosome 21 segment HS21C084
2189	7188	12288	4.31	1.0E-109	Y17123.1	NT	Human sapiens SNF5/INI1 gene, exon 6
2549	7514	12632	4.09	1.0E-109	AJ0222328.1	EST_HUMAN	TR:002197_002197 CIRCULATING CATHODIC ANTIGEN ; cw95a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to cw95a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to
2549	7514	12633	4.09	1.0E-109	AJ0222328.1	EST_HUMAN	TR:002197_002197 CIRCULATING CATHODIC ANTIGEN ;

Page 162 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2880	7515	12634	2.41	1.0E-109	4504206 NT		Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
2884	8002	13014	1.32	1.0E-109	N85180.1	EST HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3304	8315	13341	1.43	1.0E-109	AW893192.1	EST HUMAN	CM3-NN009-180400-150-f0-10 NN009 Homo sapiens cDNA
3304	8315	13342	1.43	1.0E-109	AW893192.1	EST HUMAN	CM3-NN009-190400-150-f0-10 NN009 Homo sapiens cDNA
3440	8448	13474	1	1.0E-109	AF240638.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3751	8755		2.78	1.0E-109	BE148144.1	EST HUMAN	MR0-HT0209-110400-108-a04-H10209 Homo sapiens cDNA
4023	9019	14008	4.42	1.0E-109	AI655417.1	EST HUMAN	IS89806.x1 NGI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2238930 3' similar to WP:F53A2.8 CE16100;
4038	9034	14022	0.94	1.0E-109	AA662274.1	EST HUMAN	nu83c12.s1 NCI CGAP_P'22 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN
4038	9034	14023	0.94	1.0E-109	AA662274.1	EST HUMAN	nu93c12.s1 NCI CGAP_P'22 GLUTATHIONE S-TRANSFERASE THETA 2;
4280	9273	14262	2.86	1.0E-109	4504206 NT		Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
4469	8459	14438	1.07	1.0E-109	7662083 NT		Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
3	5084	10068	0.8	1.0E-110	7545804 NT		Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
38	5118	10105	3.85	1.0E-110	5803073 NT		Homo sapiens leucine-zipper-like transcriptional regulator 1 (LZTR1), mRNA
38	5118	10106	3.85	1.0E-110	5803073 NT		Homo sapiens leucine-zipper-like transcriptional regulator 1 (LZTR1), mRNA
109	5084	10068	0.79	1.0E-110	7545804 NT		Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
282	5349	10362	0.83	1.0E-110	DB7281.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
523	5558	10561	0.78	1.0E-110	U84550.1	NT	Human dystrobrevin (DTN) gene, exon 20
1161	6165	11189	0.8	1.0E-110	5031620 NT		Homo sapiens cation receptor-like (CALCR) mRNA
1260	6258	11301	1.42	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1879	6868	11857	0.92	1.0E-110	BE378477.1	EST HUMAN	601237545r-1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3808883 5'
2005	6988		1.45	1.0E-110	BF508896.1	EST HUMAN	U1-H-B14-a05-b-05-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
2787	7788		2	1.0E-110	4503098 NT		Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2861	6258	11301	1.28	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
3013	8030						Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44), and FIP3 (FIP3) genes, complete cds
4080	9074	14062	2.65	1.0E-110	M15918.1	NT	Human autoimmune antigen small nuclear ribonucleoprotein E pseudogene
4500	9490	14468	2.09	1.0E-110	AI01723.1	EST HUMAN	0x32b10.x1 Scores_NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:1627863 3' similar to SW:N121_RAT P52591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121;
4520	8510	14494	3.28	1.0E-110	AU117812.1	EST HUMAN	AU117812.1 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'
4814	9798		2.3	1.0E-110	7662441 NT		Homo sapiens KIAA1002 protein (KIAA1002), mRNA

Page 163 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
174	5238		43.9	1.0E-111	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
198	5280	10273	1.07	1.0E-111	4758807	NT	Human sapiens ras GTPase activating protein-like (NGAP) mRNA
725	5748		2.71	1.0E-111	BF035327.1	EST_HUMAN	601458531F-1 NIH_MGC_66 Homo sapiens cDNA clone [IMAGE:3882086 5'
734	6757	10778	3.95	1.0E-111	8593092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
914	6820	10985	2.29	1.0E-111	M25142.1	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
1589	6586	11848	1.57	1.0E-111	7862177	NT	Homo sapiens KIAA0555 gene product (DKF7P434D156), mRNA
4047	9043	14032	1.17	1.0E-111	7861569	NT	Homo sapiens enkephalin B (enkB) gene, exon 4 and 3' flank and complete cds
4203	9196	14178	4.84	1.0E-111	K02268.1	NT	Human enkephalin B (enkB) gene, exon 4 and 3' flank and complete cds
605	5632	10632	0.87	1.0E-112	4501834	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
608	5633	10633	4.82	1.0E-112	U28103.1	NT	Human steroidogenic acute regulatory protein (StAR) gene, exon 6
608	5633	10634	4.82	1.0E-112	U28103.1	NT	Human steroidogenic acute regulatory protein (StAR) gene, exon 6
626	5653	10657	1.33	1.0E-112	BF509039.1	EST_HUMAN	U1-H-B14-est-g-04-0-U1.st NCI_CGAP_Sub8 Homo sapiens cDNA clone [IMAGE:30586023 3'
626	5653	10658	1.33	1.0E-112	BF509039.1	EST_HUMAN	U1-H-B14-est-g-04-0-U1.st NCI_CGAP_Sub8 Homo sapiens cDNA clone [IMAGE:30586023 3'
888	6001	11032	1.84	1.0E-112	AF157623.1	NT	Human sapiens HTRA serine protease (PRSS11) gene, complete cds
1045	6055	11083	2.53	1.0E-112	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
1645	6841	11711	3.11	1.0E-112	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1645	6641	11712	3.11	1.0E-112	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2436	7407	12524	1.26	1.0E-112	BE866859.1	EST_HUMAN	601442674F1 NIH_MGC_65 Homo sapiens cDNA clone [IMAGE:3846858 5'
3004	8022		0.72	1.0E-112	4504116	NT	Human sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3171	8187	13208	1.07	1.0E-112	BE083092.1	EST_HUMAN	RC2-BT0642-330400-021-d098 B T0842 Homo sapiens cDNA clone [IMAGE:1853625 3'
3171	8187	13209	1.07	1.0E-112	BE083092.1	EST_HUMAN	RC2-BT0642-330400-021-d098 B T0842 Homo sapiens cDNA clone [IMAGE:1853625 3'
3780	8783	13198	0.71	1.0E-112	BE076073.1	EST_HUMAN	MR2-BT0590-090300-113-fc99 B T0580 Homo sapiens cDNA clone [IMAGE:1853625 3'
4608	8995	14580	6.12	1.0E-112	AB037832.1	NT	Human sapiens mRNA for KIAA1411 protein, partial cds
4608	8995	14581	6.12	1.0E-112	AB037832.1	NT	Human sapiens mRNA for KIAA1411 protein, partial cds
733	5756	10777	7.13	1.0E-113	AI365566.1	EST_HUMAN	ac85f01.x1 Schiller meningioma Homo sapiens cDNA clone [IMAGE:1853625 3'
733	5756	10778	7.13	1.0E-113	AI365566.1	EST_HUMAN	ac85f01.x1 Schiller meningioma Homo sapiens cDNA clone [IMAGE:1853625 3'
928	5945	10979	7.7	1.0E-113	M1985.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1509	6507	11663	3.94	1.0E-113	AI365566.1	EST_HUMAN	ac85f01.x1 Schiller meningioma Homo sapiens cDNA clone [IMAGE:1853625 3'
1899	7702	11920	1.45	1.0E-113	AF24075.1	NT	Hom sapiens mRNA, complete cds
3057	8074	13087	2.19	1.0E-113	A1223948.1	NT	Hom sapiens mRNA for putative RNA helicase, 3' end
59	6139	10138	0.78	1.0E-114	Y7151.2	NT	Hom sapiens mRNA for multidrug resistance protein 3 (ABCC3)
59	5139	10139	0.78	1.0E-114	Y7151.2	NT	Hom sapiens mRNA for multidrug resistance protein 3 (ABCC3)
59	5139	10140	0.78	1.0E-114	Y7151.2	NT	Hom sapiens mRNA for multidrug resistance protein 3 (ABCC3)

Page 164 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
637	5685	10689	5.07	1.0E-114	T70551.1	EST_HUMAN	yd15c01.s1 Soares fetal liver spleen 1NF1_S Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHAGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element;
1054	6063	11093	3.1	1.0E-114	8923087 NT		Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1284	6282	11338	3.85	1.0E-114	7657629 NT		Homo sapiens thyroid tumor deletion region protein 1 (RTDR1), mRNA
1602	6598	11659	5.21	1.0E-114	6831084 NT		Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
1833	6830	11699	11.15	1.0E-114	6878073 NT		Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA
2194	7173	12294	1.31	1.0E-114	AB002374.1	NT	Human mRNA for KIAA0316 gene, partial cds
2732	5125	10114	1.1	1.0E-114	AB033102.1	NT	Human sapiens mRNA for KIAA1276 protein, partial cds
2732	5125	10116	1.1	1.0E-114	AB033102.1	NT	Human sapiens mRNA for KIAA1276 protein, partial cds
3058	8075	13088	2.52	1.0E-114	X04086.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3093	8114	13132	1.9	1.0E-114	BF205374.1	EST_HUMAN	601865932F-1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4100214 5'
3809	8809	13905	1.56	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4268	9259	14249	1.12	1.0E-114	J03171.1	NT	Human interferon-alpha receptor (HuIFN- α 1p ₈₀ Rec) mRNA, complete cds
4984	9841	14918	1.86	1.0E-114	BE275824.1	EST_HUMAN	601122173F-1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346698 5'
22	5102	10087	11.8	1.0E-115	4758111 NT		Homo sapiens HLA-B associated transcript-1 (D6S31E) mRNA
130	5196	10211	2.72	1.0E-115	45056938 NT		Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
134	5200		21.76	1.0E-115	4557887 NT		Homo sapiens keratin 18 (KRT18) mRNA
290	6347	10359	4.49	1.0E-115	AW804759.1	EST_HUMAN	QV4JU000B-200330-155-508 UM0054 Homo sapiens cDNA
778	5799	10828	1.42	1.0E-115	5174702 NT		Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
778	5799	10829	1.42	1.0E-115	5174702 NT		Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA
780	5801	10831	83.62	1.0E-115	4563794 NT		Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1528	6525	11582	1.41	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1528	6525	11583	1.41	1.0E-115	AF229180.1	NT	[Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44), and F1P3 (F1P3) genes, complete cds
1805	6786	11887	0.93	1.0E-115	U78027.1	NT	601579838F-1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2027	7010	12116	1.38	1.0E-115	BE745469.1	EST_HUMAN	601579838F-1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2027	7010	12117	1.38	1.0E-115	BE745469.1	NT	Homo sapiens testican-1 mRNA, complete cds
2236	7213	12330	3.07	1.0E-115	AF231124.1	NT	QV4JU0064-300300-156-608 UM0094 Homo sapiens cDNA
2778	7799		2.22	1.0E-115	AW804759.1	EST_HUMAN	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3041	8058	13067	7.57	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3041	8058	13068	7.57	1.0E-115	AJ245922.1	NT	Homo sapiens partial TN gene for tub
3392	8400	13426	2.06	1.0E-115	AJ277802.1	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
3929	8929	13920	5.04	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds

Page 165 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4144	9139	14123	0.86	1.0E-116	AL137763.1	NT	Novel human gene mapping to chromosome X
4278	8271	14260	1.49	1.0E-115	6912659	NT	Homo sapiens sh2-like 3 (SIRT3), mRNA
4313	8305	14289	3.78	1.0E-116	4798279	NT	Homo sapiens EPHA4 (EPHA4), mRNA
4459	9449	14429	0.91	1.0E-115	8922435	NT	Homo sapiens hypothetical protein FLJ10466 (FLJ10466), mRNA
4459	9449	14430	0.91	1.0E-115	8922435	NT	Homo sapiens hypothetical protein FLJ10468 (FLJ10468), mRNA
4639	8529	14516	2.4	1.0E-115	AL086657.1	NT	Novel human mRNA from chromosome 1, which has similarities to BA12 genes
4539	9529	14518	2.4	1.0E-115	AL096657.1	NT	Novel human mRNA from chromosome 1, which has similarities to BA12 genes
4750	9735	14721	2.89	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4750	9735	14722	2.89	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
567	5600	10599	1.39	1.0E-118	BS275502.1	EST HUMAN	601121347F NIH_MGC_20 Homo sapiens cDNA clone IMAGE:29888375 5'
792	5813	10843	1.45	1.0E-116	4507334	NT	Homo sapiens synaptotagmin 1 (SYN1), mRNA
1951	6937	12038	2.12	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT), mRNA
1951	6937	12039	2.12	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT), mRNA
1975	6960	12068	1.37	1.0E-116	AU133080	NT2RP4 Homo sapiens cDNA clone NT2RP4001228 5'	AU133080 NT2RP4 Homo sapiens cDNA clone NT2RP4001228 5'
2040	7761	12131	1	1.0E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2040	7761	12132	1	1.0E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2244	7221	12340	1.16	1.0E-116	5453941	NT	Human sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA
2279	7255		1.38	1.0E-116	U78308.1	NT	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo olfr17-40 (OR17-40) pseudogene, complete cds
2387	7358	12480	1.93	1.0E-116	A0018333.1	NT	Homo sapiens mRNA for KIAA0780 protein, partial cds
2660	7710	12731	6	1.0E-116	BS5889256.1	EST HUMAN	601513377F NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914630 5'
3101	8117	13134	5.82	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
3101	8117	13135	5.82	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
4253	9247	14231	2.06	1.0E-116	5031954	NT	Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA
4701	8992	14676	1.27	1.0E-116	AI907058.1	EST HUMAN	PM-B1135-070489-016 B1135 Homo sapiens cDNA
4995	8987	14845	0.95	1.0E-116	AI243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
554	5588	10589	1.21	1.0E-117	4826638	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1061	7738	11101	2.4	1.0E-117	AF124393.1	NT	Mus musculus (ragle-X-related protein 1 (Rxr1) gene, exons 1-3a through 15
1714	8709	11785	3.05	1.0E-117	AF123320.1	NT	Homo sapiens lymphocyte activation-associated protein 1 (Fxr1) gene, exon 10
1795	6786	11876	1.83	1.0E-117	M19816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
2149	7128	12245	1.3	1.0E-117	AW987659.1	EST HUMAN	EST369769 MAGE resequencing, MAGE_Homo sapiens cDNA
2537	7502	12921	1.04	1.0E-117	M63468.1	NT	Human alpha-5 collagen type IV gene, exon 6
3194	8210	13232	1.83	1.0E-117	AA97814.1	EST HUMAN	cp32c11.51 Scores_NEL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1578548 3'

Table 4
Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3884	8885	13885	14.06	1.0E-117	AA316723.1	EST_HUMAN	EST188414 HCC cell line (malesteris to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
4218	9211	14180	2.65	1.0E-111	8659584	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4444	9434	14417	2.36	1.0E-117	AL04220.1	EST_HUMAN	DKFZp434C1120_r1_434 (synonym: hess9) Homo sapiens cDNA clone DKFZp434C1120 5'
4584	9572	14561	1.11	1.0E-117	X88670.1	NT	H.sapiens mRNA for TPOR16 protein
4584	9572	14562	1.11	1.0E-117	X88670.1	NT	H.sapiens mRNA for TPCR16 protein
4665	9650	14638	11.6	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4665	9650	14639	11.6	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4782	9768	14750	3.85	1.0E-117	AB020873.1	NT	Homo sapiens mRNA for KIAA0868 protein, complete cds
69	5148	10155	11.76	1.0E-118	AF18150.1	NT	Homo sapiens HSPC151 mRNA, complete cds
94	5171	10181	1.94	1.0E-119	AL04554.1	EST_HUMAN	DKFZp4341058_r1_434 (synonym: hess3) Homo sapiens cDNA clone DKFZp4341058 5'
513	5548	10553	7.24	1.0E-118	78657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
803	7734	10857	6.59	1.0E-118	5174680	NT	Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA
2171	7150	12289	7.75	1.0E-118	BE389705.1	EST_HUMAN	6012818477F_NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 6'
2171	7150	12289	7.75	1.0E-118	BE389705.1	EST_HUMAN	6012818477F_NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 6'
2268	7245	12299	7.75	1.0E-118	BE389705.1	EST_HUMAN	6012818477F_NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 6'
2667	7626	12738	1.9	1.0E-118	AW851728.1	EST_HUMAN	EST363799 MAGE sequences, MAGE Homo sapiens cDNA
2667	7626	12739	3.94	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3031	8048	8048	3.94	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3122	8138	13159	4.44	1.0E-118	Y13932.1	NT	Homo sapiens PRKY exon 7
3122	8138	13160	4.93	1.0E-118	Y13769.1	EST_HUMAN	qp01f05_x1_NCI_CGAP_Kids Homo sapiens cDNA clone IMAGE:1916769 3'
3872	8970	13858	17.63	1.0E-118	D23660.1	NT	Human mRNA for ribosomal protein, complete cds
4569	9557	14545	1.42	1.0E-118	11425783	NT	Homo sapiens KIAA0478 gene product (KIAA0478), mRNA
748	6770	10797	0.93	1.0E-119	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
1020	7737	10859	4.3	1.0E-118	7705607	NT	Homo sapiens CG1-105 protein (LOC51011), mRNA
1893	6881	11972	3.42	1.0E-118	AB023147.1	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
3029	8046	13058	0.92	1.0E-119	8922205	NT	Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA
3847	8849	13887	0.86	1.0E-119	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
289	5358	10368	1.07	1.0E-120	4507334	NT	Homo sapiens synaptotagmin 1 (SYN1), mRNA
1024	6034	11055	2.23	1.0E-120	AF248840.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1024	6034	11068	2.23	1.0E-120	AF248840.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1400	6397	11452	6.07	1.0E-120	NA4873.1	EST_HUMAN	Y40g12_r1_Scares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273768 5'
1566	6563	11626	4.73	1.0E-120	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds

Page 167 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1770	6762	11850	3.83	1.0E-120	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2049	7031	12143	1.03	1.0E-120	AB011398.1	NT	Homo sapiens gene for AF-3, complete cds
2049	7031	12144	1.03	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-3, complete cds
3235	5356	10388	0.89	1.0E-120	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1) mRNA
4232	9228	14209	1.43	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4232	9226	14210	1.43	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4527	9517	14503	2.41	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
4527	9517	14504	2.41	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
72	6150	10159	2.65	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
377	5124	10439	1.27	1.0E-121	AU134983.1	EST_HUMAN	AU134983 PLACE:000899 5'
714	7728	10764	1.28	1.0E-121	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
2501	7469	12584	1.28	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4150286 5'
2501	7469	12585	1.28	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4150286 5'
2899	7918	12939	0.88	1.0E-121	AF11168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
3007	8024	13037	4.04	1.0E-121	Y19208.1	NT	Homo sapiens hB3 gene for hair keratin, exons 1 to 9
3459	8467	13494	4.04	1.0E-121	Y19208.1	NT	Homo sapiens hB3 gene for hair keratin, exons 1 to 9
3459	8467	13495	0.84	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3553	8800	13807	8.01	1.0E-121	AB165168.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
4204	9197	14179	1.34	1.0E-121	AB263284.1	EST_HUMAN	qp57501.x1 NCI CGAP_Pant Homo sapiens ECE-1 gene (exon 17)
4817	9801	14781	3.38	1.0E-121	X91937.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
5008	9979	14954	1.26	1.0E-121	AB032481.1	NT	Homo sapiens HOXD13 gene for homeobox transcription factor, complete cds
265	5324	10333	1.82	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
334	5386	10393	3.2	1.0E-122	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
356	5406	10418	1.71	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
871	5889	10931	2.93	1.0E-122	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
1200	6201	11238	3.95	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22,4) variable region (subgroup V kappa II)
1684	6850	11722	3.55	1.0E-122	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1874	6670	11746	6.77	1.0E-122	11418424	NT	Homo sapiens collagen, type XI, alpha 1 (COL12A1), mRNA
1874	6870	11747	5.77	1.0E-122	11418424	NT	Homo sapiens collagen, type XI, alpha 1 (COL12A1), mRNA
1778	6770	11862	4.64	1.0E-122	BE806024.1	EST_HUMAN	6011497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898358 5'
2420	7391	12511	20.14	1.0E-122	BF316170.1	EST_HUMAN	6011886173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126234 5'
2420	7391	12512	20.14	1.0E-122	BF316170.1	EST_HUMAN	6011886173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126234 5'

Page 168 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2766	7787	12810	0.88	1.0E-122	AF284717.1	NT	Homo sapiens FYN domain-containing dual specificity protein phosphatase FYN-E domain (protease nexin-II, Alzheimer disease) (APP), mRNA cds
4699	9684	14687	2.44	1.0E-122	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA U1-HF-BN0-all-a-03-0-UL71 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078948 5'
4832	8816		1.49	1.0E-122	AW50465.1	EST_HUMAN	602018058F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4153870 5'
759	5780	10807	2.05	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4153870 5'
759	5780	10808	2.05	1.0E-123	BF345274.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C049
997	6009	11039	5.43	1.0E-123	AL163249.2	NT	Homo sapiens inner membrane protein, mitochondrial (mitofillin) (MMT), mRNA
1006	6016	11046	6.48	1.0E-123	6803114	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B), mRNA, and translated products
1219	6218	11260	4.18	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B), mRNA, and translated products
1219	6218	11261	4.18	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B), mRNA, and translated products
1428	6425	11484	2.56	1.0E-123	AJ388844.1	NT	Homo sapiens partial mRNA for immunoglobulin kappa chain variable region (IGVK gene), sample G1N02
2042	7024	12134	1.75	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2042	7024	12135	1.75	1.0E-123	M55418.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2042	7024	12136	1.75	1.0E-123	M55418.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2251	7228		2.82	1.0E-123	77059562	NT	Homo sapiens RAB9-like protein (LOC51209), mRNA
4326	9318		0.93	1.0E-123	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
268	5325	10334	2.41	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
268	5325	10335	2.41	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
272	5331		1.29	1.0E-124	DB7675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
482	6519	10530	2.33	1.0E-124	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
682	5706	10717	5.13	1.0E-124	AA397551.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT); 281b04.1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TRG300482
682	5708	10718	5.13	1.0E-124	AA397551.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT); Human putative ribosomal protein S1 mRNA
749	6771	10798	8.09	1.0E-124	AF165654.1	NT	Human putative ribosomal protein S1 mRNA
789	5820	10890	1.42	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
893	6911	10930	2.98	1.0E-124	7705446	NT	Homo sapiens hypothetical protein (HSPC068), mRNA
1328	6326	11373	4.52	1.0E-124	AF274492.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1328	6326	11374	4.62	1.0E-124	AF274492.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1778	6771	11883	4.44	1.0E-124	AJ131712.1	NT	Homo sapiens mRNA for nucleolar RNA-helicase (noH81 gene)

Page 169 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2009	6982	12096		1.32	1.0E-124	BB878624.1	EST_HUMAN 60149715F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893954 5'
2388	7359	12481		1.32	1.0E-124	AB024069.1	Homo sapiens gene for B120, exon 11
3410	8419	13447		0.74	1.0E-124	S788694.1	Homo sapiens A1P-sensitive inwardly rectifying K-channel subunit (KCNJ6/B1R1) gene, exon
3410	8419	13448		0.74	1.0E-124	S788694.1	Homo sapiens A1P-sensitive inwardly rectifying K-channel subunit (KCNJ6/B1R1) gene, exon
3564	8571	13577		1.19	1.0E-124	X37894.1	H.sapiens lecte dehydrogenase B gene exon 1 end 2 (EC 1.1.1.27) (and joined CDS)
3804	8807	13813	0.89	1.0E-124	4507560	NT	H.sapiens T-cell lymphoma invasion and metastasis 1 (Tiam1) mRNA
3982	8960	13950	0.81	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kinain 1 (Grin1) mRNA
4601	9669	14576	2.01	1.0E-124	AB024069.1	NT	Homo sapiens gene for B120, exon 11
4778	9762		1.39	1.0E-124	M18178.1	NT	Human fibronectin gene extra type III repeat (EDII), exon x+1
317	5372		1.96	1.0E-125	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
423	5081	10065	4.13	1.0E-125	BE743922.1	EST_HUMAN 6017579881F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:38926865 5'	
718	5741	10758	1.95	1.0E-125	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
							2k53c07_s1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to
849	5868	10909		3.29	1.0E-125	AA042813.1	EST_HUMAN 9bX65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
983	5998	11028	1.63	1.0E-125	AL163210.2	NT	Homo sapiens Cironosamine 21 segment HS21C010
1136	6141	11170	1.77	1.0E-125	7662279	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
1775	6767	11858	2.38	1.0E-125	AF015450.1	NT	Homo sapiens Usompin-alpha mRNA, complete cds
1775	6767	11859	2.36	1.0E-125	AF015450.1	NT	Homo sapiens Usompin-alpha mRNA, complete cds
2297	7272	12389	2.16	1.0E-125	AA011281.1	EST_HUMAN 2k53c07_s1 Soares_fetal liver_spleen_TNF_S1 Homo sapiens cDNA clone IMAGE:4288688 5'	
2431	7402	12521	1.54	1.0E-126	AA042813.1	EST_HUMAN 9bX65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);	
2520	7487	12605	1.74	1.0E-126	4504696	NT	Homo sapiens inhibin, alpha (INHA) mRNA
2520	7487	12608	1.74	1.0E-125	4504696	NT	Homo sapiens inhibin, alpha (INHA) mRNA
							bb74f08.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048131 5' similar to TR:093604 093604
2940	10044	12978	0.88	1.0E-125	BE018009.1	EST_HUMAN ZINC FINGER PROTEIN_	
3768	8771	13776	2.21	1.0E-125	AA042813.1	EST_HUMAN 3k53c07_s1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to	
4419	9409	14396	2.44	1.0E-125	11425114	NT	bb>855857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
4419	9409	14397	2.44	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4484	9474	14454	1.81	1.0E-125	BE315412.1	EST_HUMAN 601141152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140788 5'	
765	5786	10815	1.81	1.0E-126	4758007	NT	Homo sapiens CDC-like kinase (CLK) mRNA
768	5789	10818	2.59	1.0E-126	M61938.1	NT	Human laminin B1 chain gene, exon 20
908	5925	10960	1.26	1.0E-128	X69735.1	NT	H.sapiens gene for alpha1-antichymotrypsin, exon 3
2293	7259	12377	1.21	1.0E-128	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA

Page 170 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2283	7259	12378	1.21	1.0E-126	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2521	7488	12807	2.83	1.0E-126	6382078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
2899	8017	13030	54.41	1.0E-126	AA160709.1	EST_HUMAN	z072c03.11 Stratagene pancreas (#837208) Homo sapiens cDNA clone IMAGE:592420 5'
2899	8017	13031	54.41	1.0E-126	AA160709.1	EST_HUMAN	z072c03.11 Stratagene pancreas (#837208) Homo sapiens cDNA clone IMAGE:592420 5'
3545	8552	15559	0.75	1.0E-126	X53841.1	NT	H. sapiens DNA for liver cytochrome b5 pseudogene
3571	8878	13584	2.04	1.0E-126	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
4612	9827	14619	0.98	1.0E-126	AF01108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4612	9827	14620	0.98	1.0E-126	AF01108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4687	9872	14654	1.53	1.0E-126	N34078.1	EST_HUMAN	yx78c08.11 Scores melanocyte 2Nb1M Homo sapiens cDNA clone IMAGE:287850 5'
171	5236	10247	8.83	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
171	5236	10248	8.83	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
172	5236	10247	8.4	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
172	6236	10248	8.4	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
271	5330	10342	1.45	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
271	5330	10343	1.45	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
870	6888	10930	1.36	1.0E-127	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
905	6922	10959	1.51	1.0E-127	U72621.2	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
1852	6648	11720	1.92	1.0E-127	48227053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2013	6996	12099	2.09	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2013	6996	12100	2.09	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2137	7117	12231	38.06	1.0E-127	4506620	NT	Homo sapiens ribosomal protein L26 (RPL26) mRNA
2280	7256	12374	2.58	1.0E-127	AF245565.1	NT	Homo sapiens adican mRNA, complete cds
2635	7500	12620	16.49	1.0E-127	X12881.1	NT	Human mRNA for cyokeratin 18
3606	8613	13821	0.82	1.0E-127	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
3721	8725	13725	17.44	1.0E-127	AW161297.1	EST_HUMAN	au80e06.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782694 5' similar to repetitive element;
4132	9127	14110	22.49	1.0E-127	7708239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4132	9127	14111	22.49	1.0E-127	7708239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4472	9462	14441	5.1	1.0E-127	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4498	9488	14513	3.63	1.0E-127	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4537	9527	14513	1.21	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYYBP), mRNA

Page 171 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
457	6494	10506	4.57	1.0E-128	BE385617.1	EST_HUMAN	601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:36188222 5'
2018	7001	12104	12.08	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2018	7001	12105	12.08	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2147	7126	12243	127.93	1.0E-128	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2377	7349		4.72	1.0E-128	11437455	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
3310	8321	13344	1.28	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4529	9519	14506	4.83	1.0E-128	11426673	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
122	5447	10469	1.18	1.0E-128	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
410	5447	10469	1.25	1.0E-128	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1680	6876	11750	3.33	1.0E-129	AL096890.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
1685	6681	11755	1.56	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1685	6681	11756	1.58	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1809	9799	11890	5.18	1.0E-129	11416822	NT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
3055	8072	13082	1.71	1.0E-129	Q14585	ZINC FINGER PROTEIN HF10	
3055	8072	13083	1.71	1.0E-129	Q14585	ZINC FINGER PROTEIN HF10	
3055	8072	13084	1.71	1.0E-129	Q14585	ZINC FINGER PROTEIN HF10	
4010	9006	13994	1.03	1.0E-129	6032230	NT	Homo sapiens A kinase (PRKA) anchor protein 9 (AKAP9), mRNA
4010	9006	13995	1.03	1.0E-129	5032230	NT	Homo sapiens A kinase (PRKA) anchor protein 9 (AKAP9), mRNA
4040	9038	14028	1.86	1.0E-129	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
4158	9153	14135	2.16	1.0E-129	AW755254.1	EST_HUMAN	CMY45 Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMY45
4158	9153	14136	2.16	1.0E-129	AW755254.1	EST_HUMAN	CMY45 Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMY45
75	5153	10163	1.95	1.0E-130	7705530	NT	Cardiomyopathy associated gene 5
1627	6624	11693	31.59	1.0E-130	BE275192.1	EST_HUMAN	601121955F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3448366 5'
1627	6624	11694	31.59	1.0E-130	BE275192.1	EST_HUMAN	601121955F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3448366 5'
1837	6923		2.06	1.0E-130	X04092.1	NT	Human gene for catalase (EC 1.1.1.6) exon 9 mapping to chromosome 11, band p13
2658	7655		5.31	1.0E-130	AJ010220.1	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2809	7829	12844	1.17	1.0E-130	BE564249.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885466 5'
2809	7829	12845	1.17	1.0E-130	BE564249.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885466 5'
3487	8505	13520	0.78	1.0E-130	AF240698.1	NT	Homo sapiens retina dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds

PCT/US01/00661

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3681	7829	12844	5.51	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885466 5'
3681	7829	12845	6.61	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885466 5'
3833	8835	13841	1.54	1.0E-130	AW503580.1	EST_HUMAN	UI-HF-BN0-aky-9-06-0-Ui_1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
3960	8958	13947	1.25	1.0E-130	M97770.1	NT	Human T-cell receptor (V alpha 22-1, J alpha RPM14265-variant, C alpha 1) mRNA
4408	8999	14833	9.21	1.0E-130	AW843983.1	EST_HUMAN	CMA-CN0045-180200-511-f02 CN0045 Homo sapiens cDNA
4928	9803	14880	1.3	1.0E-130	AW363289.1	EST_HUMAN	RC0-CT0318-201198-031-a11 CT0318 Homo sapiens cDNA
4928	9803	14881	1.3	1.0E-130	AW363289.1	EST_HUMAN	RC0-CT0318-201198-031-a11 CT0318 Homo sapiens cDNA
4	5085	10069	1.8	0.0E+00	AA228126.1	EST_HUMAN	Z58604.1 Soares_NHMfPu_S1 Homo sapiens cDNA clone IMAGE:367590 5' similar to TR-G222811 G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.
4	5085	10070	1.8	0.0E+00	AA228126.1	EST_HUMAN	Z58c04.1 Soares_NHMfPu_S1 Homo sapiens cDNA clone IMAGE:367590 5' similar to TR-G222811 G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.
8	5088	10074	1.14	0.0E+00	4885136	NT	Hom sapiens checkpoint suppressor 1 (CHESS1). mRNA
21	5101	10085	5.04	0.0E+00	D83227.1	NT	Hom sapiens DCRR1 mRNA, partial cds
21	5101	10086	6.04	0.0E+00	D83227.1	NT	Hom sapiens DCRR1 mRNA, partial cds
27	5107	10091	107.34	0.0E+00	AF141349.1	NT	Hom sapiens beta-tubulin mRNA, complete cds
35	5115	10101	1.77	0.0E+00	68029897	NT	Hom sapiens Cdc42 effector protein 2 (CEP2). mRNA
37	5117	10104	0.74	0.0E+00	M58600.1	NT	Human heparin cofactor II (HCFC2) gene, exons 1 through 5
41	5121	10109	24.17	0.0E+00	6857825	NT	Hom sapiens RNA-binding protein S1, serine-rich domain (RNPS1). mRNA
58	5138	10138	4.3	0.0E+00	Y1715.2	NT	Hom sapiens mRNA for multidrug resistance protein 3 (ABCC3)
58	5139	10137	4.3	0.0E+00	Y1715.2	NT	Hom sapiens mRNA for multidrug resistance protein 3 (ABCC3)
60	5140	10141	2.89	0.0E+00	D78804.1	EST_HUMAN	HUM516-H08B Human placenta polyA+ (T) Fujiwara Homo sapiens cDNA clone GEN_516H108 5'
60	5140	10142	2.89	0.0E+00	D78804.1	EST_HUMAN	HUM516-H08B Human placenta polyA+ (T) Fujiwara Homo sapiens cDNA clone GEN_516H108 5'
61	5141	10143	54.73	0.0E+00	L16558.1	NT	Human ribosomal protein L7 (RPL7) mRNA, complete cds
63	5143	10146	11.31	0.0E+00	AW06534.1	EST_HUMAN	cr48e07_x1 J1 bone marrow stroma Homo sapiens cDNA clone HBMS_C_cr48e07 3'
63	5143	10147	11.31	0.0E+00	AW06534.1	EST_HUMAN	cr48e07_x1 J1 bone marrow stroma Homo sapiens cDNA clone HBMS_C_cr48e07 3'
74	5152	10161	2.85	0.0E+00	4758977	NT	Hom sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
74	5152	10162	2.85	0.0E+00	4758977	NT	Hom sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
77	5152	10161	1.73	0.0E+00	4758977	NT	Hom sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
77	5152	10162	1.73	0.0E+00	4758977	NT	Hom sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
80	5157	10168	0.7	0.0E+00	4501850	NT	Hom sapiens amilloid binding protein 1 (amine oxidase (copper-containing)) (ABP1), nuclear gene
81	5158	10169	50.8	0.0E+00	4504444	NT	Hom sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
80	5167	10177	77.83	0.0E+00	5016088	NT	Hom sapiens actin, beta (ACTB) mRNA
93	5170	10180	45.78	0.0E+00	U89277.1	NT	Human polynemic 1 homolog (HPH1) mRNA, partial cds

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
100	5177	10187	2.36	0.0E+00	AI114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
101	6178	10188	1.89	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
116	5188	10187	0.91	0.0E+00	AI623701.1	EST_HUMAN	ts3805_x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR ;
117	5188	10187	1.65	0.0E+00	AI623701.1	EST_HUMAN	ts01h09_r1 Soares melanocyte 2nbHM Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR ;
118	7890	10188	3.4	0.0E+00	NS6040.1	EST_HUMAN	yy01h09_r1 Soares melanocyte 2nbHM Homo sapiens cDNA clone IMAGE:270017 5'
118	7890	10189	3.4	0.0E+00	NS6040.1	EST_HUMAN	yy01h09_r1 Soares melanocyte 2nbHM Homo sapiens cDNA clone IMAGE:270017 5'
121	5191	10204	0.7	0.0E+00	4505458	NT	Homo sapiens neuropilin 2 (NRP2) mRNA
131	5187	10212	4.8	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
131	5187	10213	4.8	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
140	5205	10220	1.18	0.0E+00	T66945.1	EST_HUMAN	ya83g04_r2 Strategene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 6'
140	5205	10221	1.18	0.0E+00	T56945.1	EST_HUMAN	ya83g04_r2 Strategene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 6'
152	5218	10218	70.7	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
156	5222	10234	3.22	0.0E+00	BF03681.1	EST_HUMAN	601460375f1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3163103 5'
158	5224	10239	143.39	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
161	5227	10237	0.82	0.0E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
163	5228	10238	6.28	0.0E+00	BF285573.1	EST_HUMAN	601174270f1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528664 6'
164	5229	10238	1.45	0.0E+00	BE295573.1	EST_HUMAN	601174270f1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528664 6'
165	5230	10239	6.65	0.0E+00	W73973.1	EST_HUMAN	zb62b05_r1 Soares_fetal_near_NbH19W Homo sapiens cDNA clone IMAGE:345201 5' similar to gb:X16282_cds1 ZINC FINGER PROTEIN CLONE 847 (HUMAN);
166	6231	10240	2.09	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-058-004 HT0457 Homo sapiens cDNA
166	6231	10241	2.09	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-058-004 HT0457 Homo sapiens cDNA
167	5232	10242	3.77	0.0E+00	AF244088.1	NT	Homo sapiens zinc finger protein mRNA, complete cds
170	5235	10245	15.16	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
170	5235	10246	15.16	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
180	5243	10263	9.67	0.0E+00	BE018970.1	EST_HUMAN	bb24e12_y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863854 5' similar to WP:Y57A10A_2 CE22631 ;
180	5243	10264	9.67	0.0E+00	BE018970.1	EST_HUMAN	bb24e12_y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A_2 CE22631 ;
185	5248	10257	4.23	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
185	6248	10258	4.23	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
186	6249	10259	3.83	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
186	6249	10260	3.83	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds

Page 174 of 209

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
194	62568	10271	281.78	0.0E+00	DB06898.1	NT	Human gamma-cytokeletal actin (ACTGP9) pseudogene
199	52633	10276	3.01	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen set 4-3 mRNA, complete cds
199	52633	10277	3.01	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen set 4-3 mRNA, complete cds
201	52655	10279	28.3	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
201	52655	10280	28.3	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
210	7715	10286	57.42	0.0E+00	AI587308.1	EST_HUMAN	[Q0408_X1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847.3] similar to gb:J03191 PROFILIN (HUMAN);
210	7715	10287	57.42	0.0E+00	AI587308.1	EST_HUMAN	[Q0408_X1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847.3] similar to gb:J03191 PROFILIN (HUMAN);
212	5275	10289	1.9	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
214	5277		99.79	0.0E+00	4506832	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
216	5278		15.17	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
220	5283	10293	3.41	0.0E+00	AB018264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
221	5283	10293	3.35	0.0E+00	AB018264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
222	5284	10294	4.92	0.0E+00	6678444	NT	Mus musculus testis-specific protein, Y-encoded-like (TSPY), mRNA
236	5293	10309	16.43	0.0E+00	5453805	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
238	6300		17.29	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
245	5305	03115	3.82	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
247	5307	10318	1.5	0.0E+00	X89772.1	NT	H. sapiens mRNA for interferon beta receptor (long form)
255	5315		6.35	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
267	5326	10336	1.48	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
267	5326	10337	1.48	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
269	5328	10339	2.14	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC52750).mRNA
280	5338		2.81	0.0E+00	DB3327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
281	5339	10352	2.43	0.0E+00	DB3327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
281	5339	10353	2.43	0.0E+00	DB3327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
282	5340		0.88	0.0E+00	AW845289.1	EST_HUMAN	IL2-CT0031-181198-020-B03 CT0031 Homo sapiens cDNA
291	5348	10360	5.4	0.0E+00	4857029	NT	Homo sapiens potassium inward-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
291	5348	10361	5.4	0.0E+00	4857029	NT	Homo sapiens potassium inward-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
302	5359	10371	5.25	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
303	5360	10372	4.98	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
304	7718		48.48	0.0E+00	4508728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
305	5361	10373	2.02	0.0E+00	4503914	NT	Homo sapiens phosphotriacylaminimidazole synthetase, phosphotriacylaminimidazole synthetase (GART) mRNA

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
308	5362			2.32	0.0E+00	AA480002.1	EST_HUMAN
307	5363	10374		20.77	0.0E+00	4507152	NT
308	5363	10374		22.16	0.0E+00	4507152	NT
312	5367	10378		2.2	0.0E+00	AF114488.1	NT
325	5379	10387		2.91	0.0E+00	O14887	SWISSPROT
325	5379	10388		2.91	0.0E+00	O14887	SWISSPROT
326	5380	10389		3.76	0.0E+00	7657213	NT
327	5380	10389		2.04	0.0E+00	7657213	NT
342	5394	10401		2.33	0.0E+00	5174574	NT
343	5395	10402		1.6	0.0E+00	4505256	NT
346	5398	10406		10.77	0.0E+00	4827057	NT
349	5401	10411		2.29	0.0E+00	U71600.1	NT
354	5405	10416		2.65	0.0E+00	AF231919.1	NT
354	5405	10418		2.65	0.0E+00	AF231919.1	NT
355	7719	10417		3.33	0.0E+00	AF231919.1	NT
357	5407	10419		1.13	0.0E+00	4507500	NT
360	5410	10423		1.36	0.0E+00	4503854	NT
361	5411	10424		2.25	0.0E+00	D80006.1	NT
362	5411	10424		1.75	0.0E+00	D80006.1	NT
364	5413	10426		1.21	0.0E+00	4507500	NT
375	5422	10437		2.21	0.0E+00	AU134983.1	EST_HUMAN
386	5461	10479		7.9	0.0E+00	AB028942.1	NT
387	5462	10480		7.2	0.0E+00	A1363014.1	EST_HUMAN
391	5428	10444		3.05	0.0E+00	AW754180.1	EST_HUMAN
394	5431	10447		1.12	0.0E+00	4503680	NT
395	5432	10448		2.02	0.0E+00	4503680	NT
395	5432	10449		2.02	0.0E+00	4503680	NT
396	5433	10450		1.2	0.0E+00	4503680	NT
397	5434	10451		1.19	0.0E+00	4503680	NT
397	5434	10452		1.19	0.0E+00	4503680	NT
398	5435	10453		3.59	0.0E+00	4503680	NT
398	5436	10454		3.92	0.0E+00	X74870.1	NT

H sapiens gene for RNA pol II largest subunit, exons 23-29

Table 4

Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
399	5436	10456	3.82	0.0E+00	X74870.1	NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29
400	5436	10454	3.87	0.0E+00	X74870.1	NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29
400	5436	10455	3.87	0.0E+00	X74870.1	NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29
404	5440		114.34	0.0E+00	4506608	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
417	5075	10059	1.06	0.0E+00	R17785.1	EST_HUMAN	yg09at2.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31652 5'
425	5463	10481	.2.62	0.0E+00	4503914	NT	Homo sapiens phosphotriboylglycinamide formyltransferase, phosphotriboylglycinamide synthetase, phosphotriboylaminomidazole synthetase (GART) mRNA
428	5484		36.65	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
427	5466	10482	3.49	0.0E+00	AB028842.1	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
428	5466	10483	6.44	0.0E+00	4507152	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
428	5466	10484	6.44	0.0E+00	4507152	NT	Homo sapiens SON/DNA binding protein (SON) mRNA
429	5487	10485	3.81	0.0E+00	AF183607.1	NT	Homo sapiens SON/DNA binding protein (SON) mRNA
441	5478		0.76	0.0E+00	AL1632201.2	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
443	5480	10498	3.88	0.0E+00	4557879	NT	Homo sapiens chromosome 21 segment HS21C001
448	5485		1.31	0.0E+00	AA324262.1	EST_HUMAN	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
449	5486		2.44	0.0E+00	BE254447.1	EST_HUMAN	EST27054 Cerebellum II Homo sapiens cDNA 5' end
465	6502	10512	5.86	0.0E+00	4504532	NT	60111520r1 NIH MG-16 Homo sapiens cDNA clone IMAGE:3352348 5'
465	6502	10513	5.86	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
470	6506	10520	21.4	0.0E+00	4557987	NT	Homo sapiens truncated SON protein (Son) mRNA
470	6506	10521	21.4	0.0E+00	4557987	NT	Homo sapiens keratin 18 (KRT18) mRNA
480	5517	10527	2.88	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
481	6518	10528	6.35	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
481	5518	10529	5.35	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
490	6526	10534	3.11	0.0E+00	AB03035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
492	6528	10536	1.82	0.0E+00	AU132898.1	EST_HUMAN	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4-000837 5'
500	5536	10542	4.41	0.0E+00	BE385144.1	EST_HUMAN	60127495r1 NIH MG-20 Homo sapiens cDNA clone IMAGE:36115756 5'
501	7722	10543	4.79	0.0E+00	AW598925.1	EST_HUMAN	PM0-DT0065-130400-002-c06 D10065 Homo sapiens cDNA
504	6539	10545	1.51	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
505	5540	10546	0.81	0.0E+00	8923855	NT	Homo sapiens PC326 protein (PC326) mRNA
508	5543		0.68	0.0E+00	BF373403.1	EST_HUMAN	IL2-F10159-070800-1-120-F07 F10159 Homo sapiens cDNA
616	6550	10555	4.2	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
522	7723	10559	1.9	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-h05 Homo sapiens cDNA
527	5562	10565	1.88	0.0E+00	BF028005.1	EST_HUMAN	601764856F1 1 NIH MG-33 Homo sapiens cDNA clone IMAGE:3986998 5'
532	5567	10570	1.25	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds

Page 177 of 209

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
535	5570	10573		11.98 0.0E+00	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
536	5571	10574		5.39 0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
536	5571	10575		6.39 0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
538	5573	10577		3.44 0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
539	5574	10578		2.66 0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
539	5574	10579		2.66 0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
544	5578			3.9 0.0E+00	AF0036128.1	NT	Homo sapiens X-linked anhistrolic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
552	5588	10588		1.35 0.0E+00	AW/35524.1	EST_HUMAN	U1-H-B11-acb-h-04-0-U1_s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
581	5595			4.6 0.0E+00	D10983.1	NT	Homo sapiens retrovirus-like element
581	5613	10613		7.89 0.0E+00	5174742	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCFS1), nuclear gene encoding mitochondrial protein, mRNA
594	5625			4.24 0.0E+00	J04066.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
597	5628	10627		2.06 0.0E+00	BF10488.1	EST_HUMAN	601822627F1_NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 6'
599	5630	10630		1.05 0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
599	5630	10630		1.05 0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
600	5630	10629		0.82 0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
600	5630	10630		0.92 0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
601	5630	10629		0.7 0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
601	5630	10630		0.7 0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
610	5637	10638		0.83 0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Of-interacting zinc finger protein mRNA, partial cds
610	5637	10639		0.83 0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Of-interacting zinc finger protein mRNA, partial cds
617	5644	10644		2.81 0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
619	5646	10649		2.39 0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
621	5648	10650		0.76 0.0E+00	68065918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
622	5649	10651		1.52 0.0E+00	68065918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
622	5649	10652		1.52 0.0E+00	68065918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
629	5657	10662		2.63 0.0E+00	AA398486.1	EST_HUMAN	2250c07.1 Sources: testis, NIH_Homo sapiens cDNA clone IMAGE:728732 6'
633	5661	10666		6.48 0.0E+00	D11078.1	NT	Homo sapiens RH2 gene, retrovirus-like element
638	5666			3.25 0.0E+00	4886526	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
645	5673	10678		2.37 0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
647	5675	10681		2.08 0.0E+00	6031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
650	5678	10685		3.14 0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASC1) gene, exon 8
654	5682	10688		1.1 0.0E+00	AF10839.1	NT	Human sodium/calcium exchanger isoform NaCa3 (NCX3) mRNA, complete cds

Page 178 of 209

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
654	5682	10889	1.1	0.0E+00	AF08389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
660	6687	10894	4.21	0.0E+00	48268947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
660	5687	10895	4.21	0.0E+00	48268947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
666	7728		1.79	0.0E+00	X57147.1	NT	Human endogenous retrovirus PHE.1 (ERV8)
674	56899	10708	2.88	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMG1) mRNA
678	5703	10711	16.74	0.0E+00	AB028012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
688	5712	10726	6.92	0.0E+00	7667468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1) mRNA
699	5723	10739	47.98	0.0E+00	AA814537.1	EST_HUMAN	rp49d01.s1 NCI_CGAP_Br1.1 Homo sapiens cDNA clone IMAGE:1128633 3' similar to gb:X57352
703	6727	10743	4.04	0.0E+00	M80675.1	NT	INTERFERON-INDUCIBLE PROTEIN 1-80 (HUMAN)
703	6727	10744	4.04	0.0E+00	M80675.1	NT	Human von Willebrand factor gene, exons 23 through 34
713	5737	10763	1.32	0.0E+00	5032192	NT	Human von Willebrand factor gene, exons 23 through 34
718	5742	10759	3.44	0.0E+00	AF264750.1	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
719	5742	10760	3.44	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
721	5744	10763	11.53	0.0E+00	11545800	NT	Homo sapiens hypothetical acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0779
727	5750	10771	2.72	0.0E+00	BE241577.1	EST_HUMAN	TCAAFP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0779
747	5769	10795	1.78	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
747	5769	10796	1.78	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
750	5772	10799	3.03	0.0E+00	J03164.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
750	5772	10800	3.03	0.0E+00	J03164.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
752	5774	10801	1.73	0.0E+00	AB037760.1	NT	Human sapiens mRNA for KIAA1339 protein, partial cds
753	5775	10802	1.35	0.0E+00	6912749	NT	Human sapiens zinc finger protein 212 (ZNF212) mRNA
755	7730	10804	4.57	0.0E+00	D30612.1	NT	Human sapiens mRNA for repressor protein, partial cds
756	5777	10805	5.14	0.0E+00	BEE689735.1	EST_HUMAN	601445647F NIH_MGC_65 Homo sapiens cDNA clone IMAGE:154046 5'
760	5781	10809	3.62	0.0E+00	R48915.1	EST_HUMAN	y69g08.1/r Seares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154046 5'
761	5782	10810	5.54	0.0E+00	5032088	NT	Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1) mRNA
770	5791	10819	1.61	0.0E+00	AB011389.1	NT	Homo sapiens gene for AF-6, complete cds
773	5795	10823	3.45	0.0E+00	76619865	NT	Homo sapiens KIAA0170 gene product (KIAA0170) mRNA
784	6805	10835	1.68	0.0E+00	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
784	5805	10836	1.58	0.0E+00	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
789	5810	10840	2.89	0.0E+00	X89772.1	NT	Homo sapiens mRNA for interferon alpha/beta receptor (long form)
789	5814	10844	3.13	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
793	5814	10845	3.13	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
787	5818	10849	10.62	0.0E+00	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
798	6819		8.45	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
814	6835	10870	1.57	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
815	5836	10871	2.15	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
817	5838	10873	1.84	0.0E+00	4557688	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNE1) mRNA
823	6843	10879	1.98	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNMB) mRNA, complete cds
823	5843	10880	1.98	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNMB) mRNA, complete cds
824	5844	10881	1.05	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNMB) mRNA, complete cds
829	5849	10886	1.72	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABP α) mRNA
833	6852	10891	2.11	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
833	5852	10892	2.11	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
840	5859		1.37	0.0E+00	AF027183.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
844	5863	10803	4.35	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
844	6863	10804	4.35	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
845	5884	10805	11.54	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
846	5865	10906	4.49	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
847	6866	10807	28.07	0.0E+00	4506726	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
850	5869	10910	1.1	0.0E+00	AB020171.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
850	6869	10911	1.1	0.0E+00	AB020171.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
851	5870	10912	1.78	0.0E+00	AA533272.1	EST_HUMAN	[n]68d07_s1 NCI CGAP_P-10 Homo sapiens cDNA clone IMAGE:8977453
851	5870	10913	1.78	0.0E+00	AA533272.1	EST_HUMAN	[n]68d07_s1 NCI CGAP_P-10 Homo sapiens cDNA clone IMAGE:8977453
852	5871		6.62	0.0E+00	BF877694.1	EST_HUMAN	[n]62085576F1 NIH MGIC_83 Homo sapiens cDNA clone IMAGE:42499165'
859	5875	10914	1.36	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
859	5875	10915	1.36	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
857	6876	10916	2.29	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
857	5876	10917	2.29	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
880	5899	10940	1.27	0.0E+00	AL163203.2	NT	Homo sapiens chondrocyte 21 segment HS21C003
887	5905	10945	1.4	0.0E+00	BE089592.1	EST_HUMAN	Q10-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
887	5905	10946	1.4	0.0E+00	BE089592.1	EST_HUMAN	Q10-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
897	5915	10955	2.23	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
907	6924		92.68	0.0E+00	45049858	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
910	5924		105.61	0.0E+00	45049858	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
911	6922	10892	1.65	0.0E+00	AF08947.1	NT	Homo sapiens alpha-1-antichymotrypsin precursor, mRNA, partial cds
912	5928	10883	1.39	0.0E+00	L28101.1	NT	Homo sapiens Kallistatin (P4) gene, exons 1-4, complete cds

Page 180 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
936	5953	10985	1.21	0.0E+00	M37180.1	NT	Human ras inhibitor mRNA, 3' end
937	5954	10986	6.88	0.0E+00	M37180.1	NT	Human ras inhibitor mRNA, 3' end
938	5955	10987	0.78	0.0E+00	M37180.1	NT	Human ras inhibitor mRNA, 3' end
939	5956	10988	1.65	0.0E+00	4507430	NT	Human sapiens thyrotrophic embryonic factor (TEF), mRNA
939	5956	10989	1.55	0.0E+00	4507430	NT	Human sapiens thyrotrophic embryonic factor (TEF), mRNA
947	7735	10986	1.94	0.0E+00	A1001948.1	EST_HUMAN	os98e03_s1_NICL_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
947	7735	10987	1.94	0.0E+00	A1001948.1	EST_HUMAN	os98e03_s1_NICL_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
949	5985	10989	7.69	0.0E+00	7657266	NT	Human sapiens KIAA0529 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0529), mRNA
950	5975	11009	1.89	0.0E+00	AB030568.1	NT	Human sapiens mRNA for P2P24, complete cds
968	5983	11015	1.14	0.0E+00	BF566974.1	EST_HUMAN	PM2_GN0014-050900-001-002 GN0014 Homo sapiens cDNA
968	5983	11016	1.14	0.0E+00	BF566974.1	EST_HUMAN	PM2_GN0014-050900-001-002 GN0014 Homo sapiens cDNA
968	5983	11017	1.14	0.0E+00	BF566974.1	EST_HUMAN	PM2_GN0014-050900-001-002 GN0014 Homo sapiens cDNA
969	5984	11018	1.55	0.0E+00	X52207.1	NT	Human sapiens partial c-fgr gene, exons 2 and 3
969	5984	11019	1.55	0.0E+00	X52207.1	NT	Human sapiens partial c-fgr gene, exons 2 and 3
978	6993	11026	2.93	0.0E+00	4757689	NT	Human sapiens chromosome Y chromosome-like (CDY1) mRNA
989	6003	11034	3.09	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB40) gene, complete cds
990	6004	11035	58.93	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB40) gene, complete cds
991	6004	11035	27.22	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB40) gene, complete cds
994	6007		6.92	0.0E+00	AF198490.1	NT	Human sapiens B622.1 region and MTG8 (CBFA2T1) gene, partial cds
995	6007		11.98	0.0E+00	AF198490.1	NT	Human sapiens B622.1 region and MTG8 (CBFA2T1) gene, partial cds
998	6010	11040	1.12	0.0E+00	AF111170.3	NT	Human sapiens 14q32. Jagged2 gene, complete cds; and unknown gene
999	6010	11040	1.89	0.0E+00	AF111170.3	NT	Human sapiens 14q32. Jagged2 gene, complete cds; and unknown gene
1000	6010	11042	1.74	0.0E+00	AF111170.3	NT	Human sapiens 14q32. Jagged2 gene, complete cds; and unknown gene
1001	6011	11041	6.04	0.0E+00	AF111170.3	NT	Human sapiens 14q32. Jagged2 gene, complete cds; and unknown gene
1004	6014	11044	2.62	0.0E+00	7661685	NT	Human sapiens DKEFP586M0122 protein (DKFP586M0122), mRNA
1008	6018	11048	4.81	0.0E+00	5803114	NT	Human sapiens inner membrane protein, mitochondrial (mitofillin) (IMMT), mRNA
1009	6019		4.43	0.0E+00	AA58880.1	EST_HUMAN	aa86907_s1_Striatogene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838238 3' similar to SW-PRSB_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8;
1012	6022	11052	0.8	0.0E+00	N43182.1	EST_HUMAN	EST51124_WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1012	6022	11053	0.8	0.0E+00	N43182.1	EST_HUMAN	EST51124_WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1013	6023	11054	1.08	0.0E+00	4759249	NT	Human sapiens TRAF family member-associated NFkB activator (TANK) mRNA

Page 181 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar ("Top" Hit BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1013	6023	11035	1.08	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associatd NFKB activator (TANK) mRNA
1018	6028		6.83	0.0E+00	8922833	NT	Homo sapiens hypothetical protein FLJ11186 (FLJ11186), mRNA
1030	6040	11070	10	0.0E+00	4758569	NT	Homo sapiens heat shock 70kD protein 9B (mortalin-2) (HSPA9B) mRNA
1048	6057	11085	3.04	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH16) mRNA
1048	6057	11088	3.04	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH16) mRNA
1052	6061	11090	3.88	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1052	6061	11091	3.86	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1053	6062	11092	127.96	0.0E+00	A/1245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 ('TUBA8' gene)
1055	6064		1.04	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1057	6066	11096	4.28	0.0E+00	6174394	NT	Homo sapiens alpha homolog (ABH), mRNA
1066	6074	11107	3.16	0.0E+00	4758117	NT	Homo sapiens Death associated protein 3 (DAP3), mRNA
1079	6098	11116	6.78	0.0E+00	BE005208.1	EST_HUMAN	MRO-BN0115-200300-003-H08 BN0115 Homo sapiens cDNA
1102	6109	11139	4.27	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1102	6109	11140	4.27	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1115	6121	11150	1.87	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX), mRNA
1115	6121	11151	1.87	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX), mRNA
1119	6122	11152	46.89	0.0E+00	4808712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1118	6124	11154	2.22	0.0E+00	8923280	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1121	6127	11157	37.23	0.0E+00	AE002659.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1123	6129	11158	82.18	0.0E+00	AB002659.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1124	6130	11159	4.76	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1124	6130	11160	4.76	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1127	6132	11162	4.36	0.0E+00	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC511729), mRNA
1128	6133	11163	0.86	0.0E+00	X65626.1	NT	H. sapiens AR74 gene
1128	6133	11164	0.86	0.0E+00	X95828.1	NT	H. sapiens AR74 gene
1129	6134	11165	1.23	0.0E+00	AI147630.1	EST_HUMAN	qb22d10-x1 Soares, pregnant_uerus_NbHPU Homo sapiens cDNA clone IMAGE:16970113
1131	6136	11167	3.08	0.0E+00	AB020710.1	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1138	6143	11173	0.86	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1138	6143	11174	0.86	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1139	6144	11175	1.05	0.0E+00	9886844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
1150	6154	11186	6.48	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1152	6156	11187	6.48	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1159	6163	11188	0.86	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
			14.62	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1172	6176	11209	1.01	0.0E+00	AF073289.1	NT	<i>Homo sapiens</i> Na ⁺ /H ⁺ exchanger isoform 2 (NHE2) mRNA, complete cds
1180	6181		1.32	0.0E+00	7657336	NT	<i>Homo sapiens</i> multi (E. coli) homolog 3 (MLH3) mRNA
1203	6204	11241	0.69	0.0E+00	8922693	NT	<i>Homo sapiens</i> hypothetical protein FLJ10697 (FLJ10697) mRNA
1206	6207	11244	0.89	0.0E+00	AF284750.1	NT	<i>Homo sapiens</i> ALR-like protein mRNA, partial cds
1208	6207	11245	0.89	0.0E+00	AF284750.1	NT	<i>Homo sapiens</i> ALR-like protein mRNA, partial cds
1207	6208	11246	1.65	0.0E+00	AF284750.1	NT	<i>Homo sapiens</i> ALR-like protein mRNA, partial cds
1208	7741	11247	1.09	0.0E+00	AF284750.1	NT	<i>Homo sapiens</i> ALR-like protein mRNA, partial cds
1227	6226	11272	4.89	0.0E+00	AF109718.1	NT	<i>Homo sapiens</i> chromosome 3 subtelomeric region
1228	6227	11273	2.52	0.0E+00	4503098	NT	<i>Homo sapiens</i> chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4) mRNA
1238	6238	11279	4.31	0.0E+00	4505740	NT	<i>Homo sapiens</i> prefelin 4 (PFDNA) mRNA
1247	6245		2.72	0.0E+00	Y18000.1	NT	<i>Homo sapiens</i> NF2 gene
1255	6253	11284	283.18	0.0E+00	4508718	NT	<i>Homo sapiens</i> ribosomal protein S2 (RPS2) mRNA
1282	6280	11303	5.84	0.0E+00	AF084478.1	NT	<i>Homo sapiens</i> Williams-Bailey syndrome deletion transcript 9 (WBSC9) mRNA, complete cds
1288	6288	11307	1.42	0.0E+00	AB040940.1	NT	<i>Homo sapiens</i> mRNA for KIAA1507 protein, partial cds
1288	6288	11308	1.42	0.0E+00	AB040940.1	NT	<i>Homo sapiens</i> mRNA for KIAA1507 protein, partial cds
1281	6280	11321	2.45	0.0E+00	5174748	NT	<i>Homo sapiens</i> Williams-Bailey syndrome (WBS) mRNA
1281	6280	11322	2.45	0.0E+00	5174748	NT	<i>Homo sapiens</i> Williams-Bailey syndrome (WBS) mRNA
1281	6280	11323	2.45	0.0E+00	5174748	NT	<i>Homo sapiens</i> Williams-Bailey syndrome (WBS) mRNA
1282	6281		2.35	0.0E+00	AF086166.1	NT	<i>Homo sapiens</i> protein phosphatase 2A BR gamma subunit gene, exon 5
1292	7743	11335	1.18	0.0E+00	7657529	NT	<i>Homo sapiens</i> rhabdoid tumor deletion region protein 1 (RTDR1) mRNA
1292	7743	11336	1.16	0.0E+00	7657529	NT	<i>Homo sapiens</i> rhabdoid tumor deletion region protein 1 (RTDR1) mRNA
1296	6294	11341	1.37	0.0E+00	6803146	NT	<i>Homo sapiens</i> ring finger protein 9 (RNFP9) mRNA
1297	6295	11342	2.26	0.0E+00	4508004	NT	<i>Homo sapiens</i> zinc finger protein 173 (ZNF173) mRNA
1299	6297	11343	0.67	0.0E+00	6803446	NT	<i>Homo sapiens</i> ring finger protein 9 (RNFP9) mRNA
1300	6298	11344	2.07	0.0E+00	4508004	NT	<i>Homo sapiens</i> zinc finger protein 173 (ZNF173) mRNA
1302	6300	11346	4.17	0.0E+00	AB011149.1	NT	<i>Homo sapiens</i> mRNA for KIAA0577 protein, complete cds
1303	6301	11347	8.28	0.0E+00	7661865	NT	<i>Homo sapiens</i> KIAA0170 gene product (KIAA0170) mRNA
1304	6302	11348	10.18	0.0E+00	7661865	NT	<i>Homo sapiens</i> KIAA0170 gene product (KIAA0170) mRNA
1305	6303	11349	3.67	0.0E+00	8567387	NT	<i>Homo sapiens</i> period (Drosophila) homolog 3 (PER3) mRNA
1305	6303	11350	3.67	0.0E+00	8567387	NT	<i>Homo sapiens</i> period (Drosophila) homolog 3 (PER3) mRNA
1317	6314	11363	1.22	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1375	6372	11421	1.84	0.0E+00	BE257955.1	EST_HUMAN	601109792F1 NIH MGC_16 Homo sapiens cDNA clone IMAGE:3350471 ⁵
1375	6372	11422	1.84	0.0E+00	BE257955.1	EST_HUMAN	601109792F1 NIH MGC_16 Homo sapiens cDNA clone IMAGE:3350471 ⁵
1384	6381	11431	1.51	0.0E+00	AJ250014.1	NT	<i>Homo sapiens</i> mRNA for Familial Cylindromatosis cDNA clone

Page 183 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
Q93B06_x1 Scores _testis_NH ₃ T Homo sapiens cDNA clone IMAGE:1831427 3' similar to WP:T27A16							
1392	6389	11442	1.10	0.0E+00	AI208766.1	EST_HUMAN	CE14213 ;
1393	6390	11443	2B.34	0.0E+00	6042206	NT	RAN, member RAS oncogene family-Homo sapiens cDNA clone IMAGE:1831427 3' similar to WP:T27A16
1401	6398	11453	1.69	0.0E+00	4505846	NT	Homo sapiens proprotein convertase subunit/kevin type 2 (PCSK2) mRNA
1401	6398	11454	1.59	0.0E+00	4505846	NT	Homo sapiens proprotein convertase subunit/kevin type 2 (PCSK2) mRNA
1403	6400	11457	3.9	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114) mRNA
1403	6400	11468	3.8	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114) mRNA
1405	6402	11458	4.32	0.0E+00	AJ238693.1	NT	Homo sapiens partial AF-9 gene, exons 2 to 7 and Alu repeat elements
1413	6411	11470	3.58	0.0E+00	AF038280.1	NT	Homo sapiens alpha-1-6fucosyltransferase (alpha-1-6Fuct) gene, exon 7
1434	6431	11481	2.12	0.0E+00	AL132898.1	NT	Novel human gene on chromosome 20
1435	6432	11489	1.3	0.0E+00	AL137764.1	NT	Novel human gene mapping to chromosome 1
1439	6436	11493	1.69	0.0E+00	DB7077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1442	6439	11496	6.31	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330) mRNA
1444	6441	11499	2.08	0.0E+00	7861885	NT	Homo sapiens KIAA0170 gene product (KIAA0170) mRNA
1444	6441	11499	2.08	0.0E+00	7861885	NT	Homo sapiens KIAA0170 gene product (KIAA0170) mRNA
1480	6477	11533	3.1	0.0E+00	7705434	NT	Human sapiens HDAC for homolog of Drosophila headcase (LOC51696) mRNA
1483	6491	11546	0.99	0.0E+00	AW059887.1	EST_HUMAN	EST371757 IMAGE sequences, MAGF Homo sapiens cDNA
1494	6492	11547	2.99	0.0E+00	AA481172.1	EST_HUMAN	AA481172.1 Homo sapiens cDNA clone IMAGE:815116.5'
1500	6498	11551	42.31	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1500	6498	11552	42.31	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1502	6500	11555	1.1	0.0E+00	AW976087.1	EST_HUMAN	EST37388206 IMAGE sequences, MAGN Homo sapiens cDNA
1502	6500	11556	1.1	0.0E+00	AW976087.1	EST_HUMAN	EST37388206 IMAGE sequences, MAGN Homo sapiens cDNA
1503	6501	11557	1.11	0.0E+00	D10854.1	NT	Bovine mRNA for neurocalcin
1505	8503		1.87	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44), and FIP3 (FTP3) genes, complete cds
1506	6504	11660	2.02	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMb) mRNA
1506	6504	11661	2.02	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMb) mRNA
1507	6505	11662	2.55	0.0E+00	7652405	NT	Homo sapiens KIAA0957 protein (KIAA0957) mRNA
1508	6506		7.44	0.0E+00	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1) mRNA
1613	6511	11668	3	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1616	6514	11670	1.08	0.0E+00	4507720	NT	Homo sapiens fib (TTN) mRNA
1616	6514	11571	1.08	0.0E+00	4507720	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1617			39.26	0.0E+00	4506854	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA

Page 184 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1518	6515	11572		61.77	0.0E+00	MT14984.1	NT
1530	6528	11697		8.55	0.0E+00	45030988	NT
1537	6536			1.85	0.0E+00	D00333.1	NT
1545	6543	11601		26.28	0.0E+00	283738.1	NT
1546	6544	11602		2.84	0.0E+00	5921460	NT
1548	6544	11603		2.84	0.0E+00	5921460	NT
1547	6545	11604		6.07	0.0E+00	AV690831.1	EST_HUMAN
1547	6545	11605		6.07	0.0E+00	AV690831.1	EST_HUMAN
1549	7750	11608		1.72	0.0E+00	AB040805.1	NT
1553	6550	11609		2.77	0.0E+00	AF157476.1	NT
1655	6552	11612		6.44	0.0E+00	7682183	NT
1555	6552	11613		6.44	0.0E+00	7682183	NT
1557	6554	11614		84.9	0.0E+00	61729876	NT
1557	6554	11615		84.9	0.0E+00	5728876	NT
1559	6556	11617		2.3	0.0E+00	MB1803.1	NT
1572	6569	11631		9.88	0.0E+00	H26973.1	EST_HUMAN
1579	6576	11639		1.95	0.0E+00	AB046829.1	NT
1579	6576	11640		1.95	0.0E+00	AB046829.1	NT
1593	6594	11655		4.22	0.0E+00	AV444637.1	EST_HUMAN
1625	6622	11690		8.38	0.0E+00	BE144364.1	EST_HUMAN
1625	6622	11691		8.38	0.0E+00	BE144364.1	EST_HUMAN
1629	6626	11695		3.34	0.0E+00	AI768104.1	EST_HUMAN
1630	6627	11696		1.18	0.0E+00	41759513	NT
1631	6628	11697		2.39	0.0E+00	AF057177.1	NT
1634	6631	11700		2.07	0.0E+00	M28580.1	NT
1634	6631	11701		2.07	0.0E+00	M29580.1	NT
1636	6633	11703		26.94	0.0E+00	4657987	NT
1637	6634	11704		1.45	0.0E+00	7657066	NT
1641	6638	11707		2.18	0.0E+00	BE222374.1	EST_HUMAN
1641	6638	11708		2.18	0.0E+00	BE222374.1	EST_HUMAN
1643	6639	11710		1.29	0.0E+00	4557610	NT

Page 185 of 209

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1646	6842	11713	8.67	0.0E+00	H30132.1	EST_HUMAN	ye59e08_r1 Seares breast 3NbHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:ME4099
1646	6842	11714	8.67	0.0E+00	H30132.1	EST_HUMAN	Y59e08_r1 Seares breast 3NbHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:ME4099
1648	6844	11716	19.26	0.0E+00	Z80780.1	NT	H_sapiens H2Bh gene
1648	6844	11717	19.26	0.0E+00	Z80780.1	NT	H_sapiens H2B3h gene
1651	6847		64.75	0.0E+00	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 177 (HMG17), mRNA
1680	6856	11730	5.23	0.0E+00	8823841	NT	Homo sapiens FOXJ2 forkhead factor (LOC58810), mRNA
1683	6859	11733	1.85	0.0E+00	6453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1689	6865	11741	1.1	0.0E+00	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMY1A1) mRNA
1675	6871	11748	7.62	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
1677	6873		1.82	0.0E+00	S84400.1	NT	TCR zeta (human, genomic)mRNA, 385 nt, segment 1 of 8
1688	6882	11757	1.82	0.0E+00	4557538	NT	Homo sapiens sulfate carrier family 2B (sulfate transporter), member 2 (SLC26A2) mRNA
1683	7753	11764	1.05	0.0E+00	11645911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
1706	6701	11778	2.59	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1747	7754	150.84	0.0E+00		4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1752	6746	11826	3.32	0.0E+00	4657556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1752	6746	11827	3.32	0.0E+00	4657556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1755	6748	11831	2.75	0.0E+00	U63963.1	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1759	7755	11836	8.02	0.0E+00	4505332	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
1771	6763	11851	22.05	0.0E+00	U14987.1	NT	Human ribosomal protein L21 mRNA, complete cds
1773	6765	11854	12.66	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0335 gene, partial cds
1774	6766	11855	13.86	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1774	6766	11856	13.86	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1774	6766	11857	13.86	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1788	6780	11872	1.29	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1788	6780	11873	1.29	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1788	6789	11878	5.58	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPE-1), mRNA
1788	6789	11879	5.58	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPE-1), mRNA
1807	6798	11888	3.27	0.0E+00	AB032878.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1807	6798	11889	3.27	0.0E+00	AB032878.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds

Page 186 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1811	6801	11891	3.31	0.0E+00	4826783	NT	<i>Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNCB1) mRNA</i>
1811	6801	11892	3.31	0.0E+00	4826783	NT	<i>Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNCB1) mRNA</i>
1812	6802	11893	8.06	0.0E+00	U07147.1	NT	<i>Human retinal degeneration slow (RDS) gene, exon 1</i>
1812	6802	11894	8.06	0.0E+00	U07147.1	NT	<i>Human retinal degeneration slow (RDS) gene, exon 1</i>
1815	6805	11897	1.53	0.0E+00	AW207280.1	EST_HUMAN	<i>Ui-H-B1'-atn-f-0-U1-s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'</i>
1815	6805	11898	1.53	0.0E+00	AW207280.1	EST_HUMAN	<i>Ui-H-B1'-atn-f-0-U1-s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'</i>
1837	6827	11915	2.87	0.0E+00	BE277465.1	EST_HUMAN	<i>601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547238 5'</i>
1837	6827	11916	2.87	0.0E+00	BE277465.1	EST_HUMAN	<i>601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'</i>
1878	6867	11935	1.79	0.0E+00	7657390	NT	<i>Homo sapiens nuclear protein (NP220), mRNA</i>
1878	6867	11936	1.79	0.0E+00	7657390	NT	<i>Homo sapiens nuclear protein (NP220), mRNA</i>
1881	6870	11938	2.53	0.0E+00	4506384	NT	<i>Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products</i>
1881	6870	11939	2.53	0.0E+00	4506384	NT	<i>Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products</i>
1888	6887	11987	1.87	0.0E+00	AB037788.1	NT	<i>Homo sapiens mRNA for KIAA1387 protein, partial cds</i>
1891	6880	11980	1.65	0.0E+00	AF157476.1	NT	<i>Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds</i>
1892	7758	11970	1.49	0.0E+00	M88478.1	NT	<i>Human transglutaminase mRNA, complete cds</i>
1892	7758	11971	1.49	0.0E+00	M88478.1	NT	<i>Human transglutaminase mRNA, complete cds</i>
1897	6895	11978	1.31	0.0E+00	4507464	NT	<i>Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA</i>
1897	6895	11979	1.31	0.0E+00	4507464	NT	<i>Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA</i>
1899	6897	11981	1.17	0.0E+00	7657038	NT	<i>Homo sapiens Death receptor 6 (DR6), mRNA</i>
1902	6889		6.49	0.0E+00	AF240788.1	NT	<i>Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds</i>
1907	6894		3.82	0.0E+00	M55632.1	NT	<i>Human lipoproteinase 1 pseudogene 1</i>
1908	7759	11988	1.74	0.0E+00	5901905	NT	<i>Homo sapiens butyrophillin, subfamily 3, member A2 (BTNSA2), mRNA</i>
1910	6898	11989	4.05	0.0E+00	BE01866.1	EST_HUMAN	<i>bb73f1.1y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048045 5'</i>
1916	6902	11985	1.47	0.0E+00	4809282	NT	<i>Homo sapiens histidine ammonia-lyase (HAL) mRNA</i>
1916	6902	11986	1.47	0.0E+00	4809282	NT	<i>Homo sapiens histidine ammonia-lyase (HAL) mRNA</i>
1926	6912	12007	9.5	0.0E+00	4826638	NT	<i>Homo sapiens actinin, alpha 4 (ACTN4) mRNA</i>
1926	6912	12008	9.5	0.0E+00	4826638	NT	<i>Homo sapiens actinin, alpha 4 (ACTN4) mRNA</i>
1940	6926	12023	1.41	0.0E+00	M33782.1	NT	<i>Human TFEB protein mRNA, partial cds</i>
1940	6926	12024	1.41	0.0E+00	M33782.1	NT	<i>Human TFEB protein mRNA, partial cds</i>
1942	6928	12025	1.95	0.0E+00	AW183024.1	EST_HUMAN	<i>AB69801.1x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2878913 3'</i>
1942	6928	12026	1.95	0.0E+00	AW183024.1	EST_HUMAN	<i>AB69801.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2878913 3'</i>

Page 187 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1843	6929	12027	8.45	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0350). mRNA
1843	6929	12028	8.45	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0350). mRNA
1845	6931	12030	1.25	0.0E+00	7682095	NT	Homo sapiens KIAA0408 gene product (KIAA0408). mRNA
1846	6932	12031	1.88	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1847	6933	12032	1.43	0.0E+00	Z47556.1	NT	H.sapiens genes for semenogelin I and semenogelin II
1847	6933	12033	1.43	0.0E+00	Z47556.1	NT	H.sapiens genes for semenogelin I and semenogelin II
1854	6940	12042	3.49	0.0E+00	AB040946.1	NT	Homo sapiens mRNA for KIAA513 protein, partial cds
1871	6956	12050	0.94	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1871	6956	12061	0.94	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2000	6989	12087	1.1	0.0E+00	7708742	NT	Homo sapiens TPS3TG3a (TPS3TG3a). mRNA
2004	6987	12091	13.6	0.0E+00	BE743215.1	EST_HUMAN	601673895F_NIH_MGC_9_Homo sapiens cDNA clone IMAGE:3835198 5'
2004	6987	12092	13.8	0.0E+00	BE743215.1	EST_HUMAN	601673895F_NIH_MGC_9_Homo sapiens cDNA clone IMAGE:3835198 5'
2008	6989	12093	1.98	0.0E+00	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastin component, Christmas disease, hemophilia B) (F9) mRNA
2007	6990	12094	1.02	0.0E+00	BF207688.1	EST_HUMAN	601673874F_NIH_MGC_53_Homo sapiens cDNA clone IMAGE:4081483 5'
2008	6991	12095	6.35	0.0E+00	AU140831	PLACE4_Homo sapiens cDNA clone PLACE4003921 5'	
2010	6993	12097	1.29	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7/Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2010	6993	12098	1.29	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7/Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2012	6995		2.47	0.0E+00	7687468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2014	6997		1.21	0.0E+00	4665863	NT	Homo sapiens phosphodiesterase 9A, cGMP-specific, rod, alpha (PDE6A). mRNA
2015	6998	12101	1.06	0.0E+00	Z23399.1	EST_HUMAN	HSC01C021 normalized infant brain cDNA Homo sapiens cDNA clone c-01c02
2017	7000		1.43	0.0E+00	AI244247.1	EST_HUMAN	qy60f08_x1_NCI_CGAP_U12_Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive element
2021	7004	12109	6.29	0.0E+00	BE977225.1	EST_HUMAN	601485146F_NIH_MGC_69_Homo sapiens cDNA clone IMAGE:3887747 5'
2023	7006	12111	4.71	0.0E+00	BF315225.1	EST_HUMAN	601902604F_NIH_MGC_19_Homo sapiens cDNA clone IMAGE:4135320 5'
2023	7006	12112	4.71	0.0E+00	BF315225.1	EST_HUMAN	601902604F_NIH_MGC_19_Homo sapiens cDNA clone IMAGE:4135320 5'
2028	7011	12118	2.79	0.0E+00	BE697725.1	EST_HUMAN	RC3-C10413-270700-022-010 CT0413 Homo sapiens cDNA
2028	7011	12119	2.79	0.0E+00	BE697725.1	EST_HUMAN	RC3-C10413-270700-022-010 CT0413 Homo sapiens cDNA
2033	7016	12125	2.04	0.0E+00	LO0620.1	NT	Human plasma membrane calcium ATPase Isoform 2 (ATP2B2) mRNA, complete cds
2033	7016	12126	2.04	0.0E+00	LO0620.1	NT	Human plasma membrane calcium ATPase Isoform 2 (ATP2B2) mRNA, complete cds
2036	7019	12129	1.7	0.0E+00	4768489	NT	Human sapiens GTP binding protein 1 (GTPBP1) mRNA
2055	7037		2.76	0.0E+00	BE76784.1	EST_HUMAN	QV1-GN0058-140800-318->10 GN0065_Homo sapiens cDNA
2056	7038		1.41	0.0E+00	AF018863.1	NT	Human sapiens X-linked juvenile retinoschisis protein (XLRS1) gene, exon 6 and complete cds
2059	7040	12149	4.46	0.0E+00	BF027582.1	EST_HUMAN	601672068F_NIH_MGC_20_Homo sapiens cDNA clone IMAGE:3854785 5'

Page 188 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2059	7041	12150	1.77	0.05+00	BE072624.1	EST_HUMAN	PM0-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA genes, complete cds
2061	7043	12161	2.11	0.05+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
2082	7044	12152	3.84	0.05+00	AW752708.1	EST_HUMAN	IL3-C10219-271089-022-G10 CT0219 Homo sapiens cDNA genes, complete cds
2084	7046	12154	4.62	0.05+00	AI904640.1	EST_HUMAN	QV-BT065-020389-092 BT065 Homo sapiens cDNA genes, complete cds
2084	7046	12155	4.62	0.05+00	AI904640.1	EST_HUMAN	QV-BT085-020399-092 BT085 Homo sapiens cDNA genes, complete cds
2118	7086		1.21	0.05+00	L14787.1	NT	Human DNA-binding protein mRNA, 3' end
2122	7102	12214	1.93	0.05+00	BE214653.1	EST_HUMAN.	60122338F11NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346688 5'
2124	7104	12217	1.01	0.05+00	D87685.1	NT	Human mRNA for KIAA0244 gene, partial cds
2125	7105	12218	42.14	0.05+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CENB1DE08 5'
2125	7105	12219	42.14	0.05+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CENB1DE08 5'
2127	7107	12221	3.7	0.05+00	AA891691.1	EST_HUMAN	0032601_s1 NC1_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1667896 3'
2128	7109		1.02	0.05+00	M189288.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 22 through 29
2132	7112	12226	52.74	0.05+00	BF344434.1	EST_HUMAN	602014828F11NC1_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150734 5'
2133	7113	12228	55.46	0.05+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
2136	7116	12229	4.45	0.05+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2136	7116	12230	4.45	0.05+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2140	7784	12235	4.41	0.05+00	BF313617.1	EST_HUMAN	601900281F11 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128822 5'
2143	7122	12238	2.4	0.05+00	BE018760.1	EST_HUMAN	bb984502_Y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR015170 Q15170
2145	7124	12240	2.17	0.05+00	AA042813.1	EST_HUMAN	TRANSCRIPTION FACTOR SII-RELATED PROTEIN 1 215307_s1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to
2145	7124		2.17	0.05+00	AA042813.1	EST_HUMAN	gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN); 265307_s1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to
2153	7132	12241	2.17	0.05+00	AA042813.1	EST_HUMAN	gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2153	7132	12249	2.86	0.05+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2153	7132	12250	2.86	0.05+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2154	7133	12251	2.34	0.05+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2154	7133	12252	2.34	0.05+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2159	7138	2.31	0.05+00	U36284.1	NT	Human beta-prime-adipin (BAM22) gene, exon 16	
2160	7139	12257	1.43	0.05+00	AA282281.1	EST_HUMAN	z12510_r1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712891 5'
2167	7146	12263	2.22	0.05+00	BEE897487.1	EST_HUMAN	601432317F11 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
2180	7159	12278	8.49	0.05+00	4557656	NT	Human sapiens E1A binding protein p300 (EP300) mRNA
2185	7164	12284	1.89	0.05+00	7662401	NT	Human sapiens KIAA0952 protein (KIAA0952), mRNA
2191	7170	12281	6.09	0.05+00	BE695281.1	EST_HUMAN	60143325F11 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918307 5'

Page 189 of 209
Table 4
Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2195	7174	12295	2.37	0.0E+00	BE905633.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2195	7174	12296	2.37	0.0E+00	BE905633.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2197	7175	12298	3.61	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2237	7214	12331	3.29	0.0E+00	115a5748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEEF6), mRNA
2237	7214	12332	3.29	0.0E+00	115a5748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEEF6), mRNA
2238	7216	12333	2.27	0.0E+00	AI076404.1	EST_HUMAN	0209c07_x1 Seares fetal liver spleen 1NFEL_S_1 Homo sapiens cDNA clone IMAGE:1674828 3'
2241	7218	12336	3.84	0.0E+00	AA428001.1	EST_HUMAN	zv8@11.1r1 Seares total fetus Nb2hIF8_8W Homo sapiens cDNA clone IMAGE:759740 5'
2241	7218	12337	3.84	0.0E+00	AA428001.1	EST_HUMAN	zv7@11.1r1 Seares total fetus Nb2hIF8_8W Homo sapiens cDNA clone IMAGE:759740 5'
2243	7220	12339	3.72	0.0E+00	BI347038.1	EST_HUMAN	602021846F1 NCI CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4167339 5'
2249	7225	12345	1.02	0.0E+00	6325468	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2255	7232	12381	2.79	0.0E+00	BE976095.1	EST_HUMAN	7122a02_x1 NCI CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3298370 3' similar to TR:OB4639 OB4939
2259	7235	12383	16.03	0.0E+00	AF044571.1	NT	Homo sapiens phosphatase kinase alpha subunit (PKHA2) gene, exon 32
2259	7236	12354	1.78	0.0E+00	AI655542.1	EST_HUMAN	657c08_x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:22831182 3'
2261	7238	12355	1.16	0.0E+00	AB011388.1	NT	Homo sapiens gene for AF-8, complete cds
2284	7241	12357	3.07	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2284	7241	12359	3.01	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2267	7244	12361	3.48	0.0E+00	6803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2267	7244	12382	3.48	0.0E+00	6803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2273	7249	12385	2.22	0.0E+00	7682007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2273	7249	12386	2.22	0.0E+00	7682007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2277	7253	12371	1.4	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2277	7253	12372	1.4	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2281	7263	12380	2.25	0.0E+00	5174678	NT	Homo sapiens signal regulatory protein, beta 1 (SIRP-BETA-1) mRNA
2291	7268	12384	3.98	0.0E+00	AI131142.1	EST_HUMAN	AI131142_N12RP3 Homo sapiens cDNA clone NT2RP3002064 5'
2292	7267		47.81	0.0E+00	BE794026.1	EST_HUMAN	601585845F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:38941003 5'
2293	7268	12385	2.44	0.0E+00	AW867076.1	EST_HUMAN	MR1-SN0033-120400-002-804 SN0033 Homo sapiens cDNA
2294	7269	12386	4.95	0.0E+00	7682017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2295	7270	12387	2.03	0.0E+00	4768497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2295	7270	12388	2.03	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2298	7271		4.1	0.0E+00	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 7 (CYP3A7) genes, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2298	7273	12390	21.6	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'

Page 190 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2298	7273	12391		21.5 0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2299	7273	12392		21.5 0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2299	7274	12393		1.24 0.0E+00	89223089	NT	Homo sapiens hypothetical protein FLJ20081 (FLJ20081), mRNA
2316	7281			1.61 0.0E+00	BE814424.1	EST_HUMAN	MRO-BN0070-090608-0-029-d12 BN0070 Homo sapiens cDNA
2348	7322	12441		0.99 0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2349	7323			3.28 0.0E+00	AI042035.1	EST_HUMAN	0x60502.x1 Seraes, NHMPU_S1 Homo sapiens cDNA clone IMAGE:1660683 3' similar to TR:008862
2350	7324	12442		1.18 0.0E+00	89223620	NT	008662 230 KDA PHOSPHATIDYLINOSITOL-4-KINASE :
2354	7328			4.15 0.0E+00	BE893605.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20083 (FLJ20083), mRNA
2365	7339			3.39 0.0E+00	AB005622.1	EST_HUMAN	AB005622 Hele cDNA (7'Name) Homo sapiens cDNA similar to adenylyl kinase isozyme 2
2369	7342	12460		5.63 0.0E+00	60056002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2372	7344	12463		1.57 0.0E+00	D85606.1	NT	Homo sapiens gene for cholecytokinin type-A receptor, complete cds
2372	7344	12464		1.57 0.0E+00	D85606.1	NT	Homo sapiens gene for cholecytokinin type-A receptor, complete cds
2380	7352	12473		1.34 0.0E+00	AF106227.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2384	7365	12477		0.86 0.0E+00	BF345274.1	EST_HUMAN	602018058F1 NCI CGAP_Bm87 Homo sapiens cDNA clone IMAGE:415387 5'
2390	7361	12484		6.99 0.0E+00	5729777	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2398	7369	12490		16.53 0.0E+00	BF569144.1	EST_HUMAN	60218455871 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:43003383 3'
2407	7378	12497		2.46 0.0E+00	AW468622.1	EST_HUMAN	he04n04_x1 NCI CGAP_K1412 Homo sapiens cDNA clone IMAGE:2872759 3'
2409	7380	12498		2.09 0.0E+00	AW501010.1	EST_HUMAN	UI-HF-BP0p-as-c-07-0-JI/11 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 6
2433	7404			2.13 0.0E+00	AW813653.1	EST_HUMAN	RC3-ST0187-360300-016-c04 ST0187 Homo sapiens cDNA
2438	7409	12528		27.9 0.0E+00	BE795542.1	EST_HUMAN	801162530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5'
2439	6887	11981		1.18 0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
2440	7410	12527		1.33 0.0E+00	BF509442.1	EST_HUMAN	UI-H-B14-a02-b-08-0-UI-s1 NCI CGAP_Subb Homo sapiens cDNA clone IMAGE:3086535 3'
2443	7413	12529		3.32 0.0E+00	Z32684.2	NT	Homo sapiens mRNA for membrane transport protein (XK gene)
2445	7415			3.21 0.0E+00	5453871	NT	Homo sapiens platelet-derived growth factor-like (PDGFL) mRNA
2448	7418	12533		1.05 0.0E+00	BE810378.1	EST_HUMAN	6011503356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3805148 5'
2449	7419	12534		2.35 0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2450	7420	12535		0.91 0.0E+00	BE160865.1	EST_HUMAN	RC4-HT0276-160200-013-d05 HT0276 Homo sapiens cDNA
2451	7421	12536		3.02 0.0E+00	U93239.1	NT	Human Sec62 (Sec62) mRNA, complete cds
2457	7427	12542		2.2 0.0E+00	BE886460.1	EST_HUMAN	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909866 5'
2461	7430	12547		4.05 0.0E+00	BE87551.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2461	7430	12548		4.05 0.0E+00	BE87551.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2462	7431	12549		1.27 0.0E+00	AF114027.1	EST_HUMAN	AF114027 Homo sapiens lung fetus Homo sapiens cDNA clone ESF6
2464	7433	12552		1 0.0E+00	AF246505.1	NT	Homo sapiens adican mRNA, complete cds

Page 191 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2480	7449	12560	1.91	0.0E+00	BE636921.1	EST_HUMAN	601084738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2485	7453	12567	3.77	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y78AA1 Homo sapiens cDNA clone Y78AA1 001673 5'
2485	7453	12568	3.77	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y78AA1 Homo sapiens cDNA clone Y78AA1 001673 5'
2486	7454	12569	3.86	0.0E+00	BE282898.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887866 5'
2486	7454	12570	3.86	0.0E+00	BE282898.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887865 5'
2487	7455	12571	0.93	0.0E+00	BF223041.1	EST_HUMAN	7427H12.1 NT1_NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3' similar to TR:000248 O00248
2490	7458	12573	5.98	0.0E+00	AF245605.1	NT	Homo sapiens adican mRNA, complete cds
2508	7478	12591	0.91	0.0E+00	BE286131.1	EST_HUMAN	601173651F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528159 5'
2522	7708	12608	1.49	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2522	7708	12609	1.49	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2523	7489	12614	1.85	0.0E+00	BF513835.1	EST_HUMAN	U1-H-BW1-amp-F-12-O-Ui-s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2628	7494	12614	1.25	0.0E+00	BF672818.1	EST_HUMAN	6021526553F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283612 5'
2630	7496	1.1	0.0E+00	BE616805.1	EST_HUMAN	601279873F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3621786 5'	
2339	7504	12623	2.22	0.0E+00	AB037742.1	NT	Homo sapiens mRNA for KIAA1321 protein, partial cds
2540	7505	12624	2.36	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, I, II&III (TAF2)
2542	7507	12626	5.06	0.0E+00	AB037859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
2543	7508	12627	1.42	0.0E+00	BE795445.1	EST_HUMAN	601580108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2543	7509	12628	1.42	0.0E+00	BE795445.1	EST_HUMAN	601580108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2546	7511	12629	1.35	0.0E+00	BE283328.1	EST_HUMAN	601143722F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051389 5'
2553	7518		6.42	0.0E+00	BE792472.1	EST_HUMAN	601584820F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'
2555	7620	12631	1.08	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA093 protein, partial cds
2563	7522	12645	2.7	0.0E+00	45046865	NT	Homo sapiens MP (inosine monophosphate) kinase 1 (IMPDH1) mRNA
2574	7637	12653	4	0.0E+00	AF173227.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCAT1B) gene, exon 1
2577	7540	12654	1.3	0.0E+00	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
2680	7543	12657	1.88	0.0E+00	AU133385.1	EST_HUMAN	AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP4001984 5
2581	7544	12658	1.75	0.0E+00	M69225.1	NT	Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds
2584	7547	12661	2.23	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2584	7547	12662	2.23	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000778 5'
2587	7550	12665	1.36	0.0E+00	AW887015.1	EST_HUMAN	RC1-OT0086-22030-011-4d07 OT0086 Homo sapiens cDNA
2590	7553	12668	1.01	0.0E+00	BF000018.1	EST_HUMAN	7h18h05.1 NT1_NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316089 3'
2591	7554	12669	5.22	0.0E+00	BE383185.1	EST_HUMAN	601286714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5'
2592	7556		8.33	0.0E+00	BE531283.1	EST_HUMAN	601278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3810287 5'

Page 192 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2816	7578	12690	1.38	0.0E+00	8922849	NT	Homo sapiens hypothetical protein FLJ11052 (FLJ11052), mRNA
2826	7586	12698	1.22	0.0E+00	AB037732.1	NT	Homo sapiens mRNA for KIAA1311 protein, partial cds EST:188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2850	7610		27.94	0.0E+00	AA316723.1	EST_HUMAN	601989625F NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943591 5'
2851	7611	12721	1.31	0.0E+00	BE794894.1	EST_HUMAN	601989625F NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943591 5'
2855	7615	12726	5.13	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 6
2856	7616	12727	5.03	0.0E+00	7669517	NT	Homo sapiens neuregulin 1 (NRG1), transcript variant SMDF, mRNA
2857	7617	12728	2.44	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FLH-1) gene, complete cds
2858	7618	12729	1.27	0.0E+00	AB051926.1	NT	Homo sapiens hG28K mRNA for GTP-binding protein like 1, complete cds
2864	7623	12735	26.29	0.0E+00	BE798576.1	EST_HUMAN	601581981F NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2865	7624	12736	1.5	0.0E+00	BF7680632.1	EST_HUMAN	6021555923F NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297132 5'
2868	7778	12740	24.53	0.0E+00	BE663433.1	EST_HUMAN	601335485F NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3889564 5'
2869	7627		2.28	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB-Homo sapiens cDNA clone HTBB7E09 5'
2871	7628	12743	2.82	0.0E+00	5174486	NT	Homo sapiens spermatoogenesis associated PD1 (KIAA0757) mRNA
2871	7629	12744	2.82	0.0E+00	6174486	NT	Homo sapiens spermatoogenesis associated PD1 (KIAA0757) mRNA
2872	7630	12745	1.27	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2872	7630	12746	1.27	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2873	7631	12747	2.26	0.0E+00	AF280195.1	NT	Homo sapiens hyperpension-related calcium-regulated gene mRNA, complete cds
2874	7632		51.51	0.0E+00	AV651066.1	EST_HUMAN	AV651066 GLC Homo sapiens cDNA clone GLCCLD07 3'
2875	7633	12748	3.33	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-2509800-498-008 TN0141 Homo sapiens cDNA
2875	7633	12749	3.33	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-2509800-498-008 TN0141 Homo sapiens cDNA
2682	7640	12756	19.66	0.0E+00	BF747193.1	EST_HUMAN	601580503F NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 5'
2687	7845	12760	3.09	0.0E+00	BF037713.1	EST_HUMAN	60146203871 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3885487 5'
2695	7653		0.93	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2696	7654	12768	2.63	0.0E+00	BF514110.1	EST_HUMAN	UI-H-BW1-amw-a-07-0-11 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'
2703	7660		2.14	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSFG4), mRNA
2708	7665	12776	1.05	0.0E+00	7705275	NT	Homo sapiens angiopoietin-3 (ANG-3), mRNA
2708	7665	12777	1.05	0.0E+00	7705276	NT	Homo sapiens angiopoietin-3 (ANG-3), mRNA
2709	7666	12778	2.68	0.0E+00	BF877694.1	EST_HUMAN	602085579F NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248915 5'
2715	7672	12786	1.43	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2719	7676	12789	26.73	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCCA03 5'
2719	7676	12790	26.73	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCCA03 5'
2721	7678		11.75	0.0E+00	AI879163.1	EST_HUMAN	ai5d041 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2818683 5' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13a;

Page 163 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2724	7681	12785	2.71	0.0E+00	BF530668.1	EST_HUMAN	802071857/1 NCI_GAP_Bm67 Homo sapiens cDNA clone IMAGE:4244679 5'
2725	7682	12786	58.63	0.0E+00	BE872768.1	EST_HUMAN	801450912/1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3854842 5'
2727	7684	12787	2.2	0.0E+00	AU131494.1	EST_HUMAN	AU131494_NTRP3 Homo sapiens cDNA clone NT2RP3029872 5'
2727	7684	12788	2.2	0.0E+00	AU131494.1	EST_HUMAN	AU131494_NTRP3 Homo sapiens cDNA clone NT2RP3029872 5'
2728	7685	12789	68.47	0.0E+00	BE5300344.1	EST_HUMAN	6009447194/1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860806 5'
2728	7685	12800	68.47	0.0E+00	BE5300344.1	EST_HUMAN	6009447194/1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860806 5'
2734	5251	10262	2.82	0.0E+00	ST76830.1	NT	Glycoprotein D=Duffy group antigen [human, blood, Genomic DNA, 3088 m]
2737	7682	3.43	0.0E+00	AB033281.1	NT	Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds	
2743	5747	10768	1.92	0.0E+00	Af284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2743	5747	10769	1.92	0.0E+00	Af284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2747	6032	11082	2.78	0.0E+00	4503202.1	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile)
2747	6032	11083	2.78	0.0E+00	4503202.1	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile)
2762	7783	12808	5.17	0.0E+00	X855980.1	NT	H.sapiens serine hydroxymethyltransferase pseudogene (CYP1B1) mRNA
2763	7784		1.34	0.0E+00	AF0688624.1	NT	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds
2765	7785		1.35	0.0E+00	AB040980.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2771	7792		1.16	0.0E+00	AJ238852.1	NT	Homo sapiens partial rpl3 gene for ribosomal protein L3, U82 snoRNA, U83a snoRNA and U83b snoRNA genes
2772	7793	12813	2.35	0.0E+00	AL163201.2	NT	Human sodium channel mRNA
2775	7798	12815	1.41	0.0E+00	M918031.1	NT	Human AHNAK nucleoprotein mRNA, 5' end
2777	7798	12817	1.6	0.0E+00	M80902.1	NT	H.sapiens id3 gene for HLH-type transcription factor
2781	7802		1.42	0.0E+00	X73428.1	NT	Homo sapiens chromosome 21 segment HS21C088
2783	7804		2.78	0.0E+00	AL163208.2	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2784	7805	12821	1.41	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2784	7805	12822	1.41	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2784	7805	12823	1.41	0.0E+00	7019584	NT	Homo sapiens transglutaminase mRNA, complete cds
2787	7808	12825	0.83	0.0E+00	M98478.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2792	7812	12826	38.19	0.0E+00	D50857.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2792	7812	12830	36.19	0.0E+00	D50857.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2795	7815	12833	4.89	0.0E+00	AL0986657.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2798	7816		6.12	0.0E+00	Y10858.1	NT	H.sapiens mRNA for nuclear DNA helicase II
2797	7817		1.14	0.0E+00	AF52203.1	NT	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2798	7818	12834	71.64	0.0E+00	4503470	NT	Homo sapiens sulkanyutto transistion elongation factor 1 alpha 1 (EEF1A1) mRNA

Page 194 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit No.	Top Hit Database Source	Top Hit Descriptor
2798	7818	12835	71.84	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2810	7830	12846	2.53	0.0E+00	4607280	NT	Homo sapiens actin/throcline kinase (STK9) mRNA
2813	7833	12850	1	0.0E+00	AL047599.1	EST_HUMAN	DKFZp586G0821_r1 586 (synonym: hule1) Homo sapiens cDNA clone DKFZp586G0821
2814	7834		2.12	0.0E+00	4503098	NT	Homo sapiens chondrolin sulfate proteoglycan 4 (melanoma-associated) (CSPG4) mRNA
2817	7837	12852	6.88	0.0E+00	BE081896.1	EST_HUMAN	Q12-BT0638-13040-138-103 BT0638 Homo sapiens cDNA
2817	7837	12853	5.88	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0638-13040-138-103 BT0638 Homo sapiens cDNA
2822	7843	12861	0.85	0.0E+00	68008918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2) mRNA
2822	7843	12862	0.85	0.0E+00	68008918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2) mRNA
2825	7846	12866	3.1	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment 1-521006
2825	7849	12867	3.1	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment 1-521006
2826	7847	12868	1.03	0.0E+00	AA215578.1	EST_HUMAN	zr86b11.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683517 3' similar to contains Ali repetitive element
2834	7854		4.09	0.0E+00	Y19210.1	NT	Homo sapiens hrb5 gene for hair keratin, exons 1 to 9
2836	7856	12875	1.08	0.0E+00	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
2837	7857	12876	60.46	0.0E+00	4603470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2838	7858	12877	2.63	0.0E+00	AI561002.1	EST_HUMAN	In18d07_x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167881 3' similar to TR:O16247
2838	7858	12878	2.63	0.0E+00	AI561002.1	EST_HUMAN	In18d07_x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167881 3' similar to TR:O16247
2840	7858	12880	1.19	0.0E+00	PS2740	SWISSPROT	ZINC FINGER PROTEIN_132
2841	7861	12881	1.05	0.0E+00	AF152238.1	NT	Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2857	7877	12893	2.2	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2857	7877	12894	2.2	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2858	7878	12895	5.42	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2858	7878	12896	5.42	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2861	7881	12899	2.79	0.0E+00	7861903	NT	Homo sapiens KIAA0100 gene product (KIAA0100) mRNA
2861	7881	12900	2.79	0.0E+00	7861903	NT	Homo sapiens KIAA0100 gene product (KIAA0100) mRNA
2862	7882	12901	3.2	0.0E+00	6174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2862	7882	12902	3.2	0.0E+00	6174574	NT	(MLLT4) mRNA
2867	7886	12906	0.99	0.0E+00	BF110702.1	EST_HUMAN	Tn4dd03_x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q8VLN1 CG7283 PROTEIN.

Page 195 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2867	7886	12807	0.89	0.0E+00	BF110702.1	EST_HUMAN	7n4d03_x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3587028 3' similar to TR:Q8VLN1
2875	7894	12917	2.17	0.0E+00	4505084 NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4); mRNA	
2875	7894	12918	2.17	0.0E+00	4505084 NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4); mRNA	
2882	7801	12923	1.85	0.0E+00	4758827 NT	Homo sapiens neurexin III (NRXN3) mRNA	
2883	7802		1.14	0.0E+00	X08494.1 NT	H. sapiens mRNA for M phase phosphoprotein 10	
2886	7905	12926	0.93	0.0E+00	AB0330334.1 NT	Homo sapiens mRNA for KIAA1208 protein, partial cds	
2888	7807	12927	0.94	0.0E+00	X16309.1 NT	H. sapiens NF-H gene, exon 4	
2888	7807	12928	0.94	0.0E+00	X16309.1 NT	H. sapiens NF-H gene, exon 4	
2890	7890	12930	8.37	0.0E+00	AF106275.1 NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6	
2904	7923		1.38	0.0E+00	AI149850.1 NT	qf4310B_x1 Scores. testis_NiHT Homo sapiens cDNA clone IMAGE:1752809 3'	
2912	7891	12850	1.21	0.0E+00	4506118 NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA	
2913	7892	12891	4.29	0.0E+00	AB004984.1 NT	Homo sapiens mRNA for PRK-U-alpha, partial cds	
2924	7943	12959	2.03	0.0E+00	7662273 NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA	
2925	7844	12860	2.05	0.0E+00	6729756 NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA	
2925	7844	12981	2.05	0.0E+00	6729755 NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA	
2935	7854	12971	1.3	0.0E+00	AF114488.1 NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	
2935	7854	12972	1.3	0.0E+00	AF114488.1 NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	
2953	7977	12982	1.23	0.0E+00	MT4098.1 NT	Human displacement protein (CCAA1) mRNA	
2967	7895	12899	0.84	0.0E+00	AW976286.1 EST_HUMAN	EST388375 MAGE sequences, MAGN Homo sapiens cDNA	
2970	7898		4.06	0.0E+00	AF198953.1 NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds	
2973	7891	13005	6.1	0.0E+00	6579469 NT	Homo sapiens heat shock 70kD protein 1 (HSP70A), mRNA	
2973	7891	13006	6.1	0.0E+00	6579469 NT	Homo sapiens heat shock 70kD protein 1 (HSP70A), mRNA	
2975	7893		8.5	0.0E+00	AL365403.1 NT	Isform 2 of a novel human mRNA from chromosome 22	
2979	7897	13010	1.96	0.0E+00	AF017433.1 NT	Homo sapiens putative transcription factor CR65 (CR55) mRNA, partial cds	
2982	8000		1.97	0.0E+00	AF198779.1 NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM5 protein, T54 protein, complete cds; and L-type calcium channel 8>	
3002	8020	13033	3.21	0.0E+00	X03529.1 NT	Human germline gene 16.1 for Ig lambda L-chain C region (gl-C16.1)	
3008	8025		1.81	0.0E+00	AF188355.1 NT	Homo sapiens F-box protein FB15 (FB15) mRNA, complete cds	
3012	8029	13040	1.43	0.0E+00	AF064589.1 NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds	
3033	8050	13059	3.49	0.0E+00	AF265208.1 NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds	
3034	8051	13060	6.9	0.0E+00	AF149773.1 NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	
3038	8055	13063	3.23	0.0E+00	7882139 NT	Homo sapiens KIAA0468 gene product (KIAA0468), mRNA	

Page 196 of 209
 Table 4
 Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3039	8058	13064	1.38	0.0E+00	AF042076.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
3068	8084	13098	3.44	0.0E+00	4828783	NT	Human sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNCB1) mRNA
3077	8093	13107	28.05	0.0E+00	LC0941.1	NT	Human ferritin heavy chain mRNA, complete cds
3080	8096	13110	1.09	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3080	8096	13111	1.09	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3087	8103	13118	33.16	0.0E+00	T94870.1	EST_HUMAN	ye2203.s1 Strategene lung (#93/210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP:S28539
3102	8118	13136	1.16	0.0E+00	T94870.1	EST_HUMAN	S28539 BASIC PROTEIN, 23K -
3104	8120	13137	1.26	0.0E+00	AB24336.1	EST_HUMAN	601878507F_NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107433 5'
3109	8125	13144	4.08	0.0E+00	AB1868086.1	EST_HUMAN	WU12H10_X1_NCI_OCSAP_GCSB Homo sapiens cDNA clone IMAGE:2516803 3'
3109	8125	13145	4.08	0.0E+00	X088922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3120	8136	13157	1.48	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
3120	8136	13158	1.49	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
3127	8143	13164	9.09	0.0E+00	45046368	NT	Homo sapiens interleukin 1 receptor, type I(ILR1) mRNA
3145	8161	13182	12.76	0.0E+00	M28698.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3149	8165	13185	10.04	0.0E+00	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenosine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
3155	8171	13183	0.8	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3155	8171	13184	0.8	0.0E+00	4768055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3157	8173	13195	2.91	0.0E+00	AA1774283.1	EST_HUMAN	aa87611.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3'
3165	8181	13203	5.5	0.0E+00	AF288598.1	NT	Homo sapiens angiostatin binding protein 1 mRNA, complete cds
3165	8181	13204	5.5	0.0E+00	AF288598.1	NT	Homo sapiens angiostatin binding protein 1 mRNA, complete cds
3175	8191	13212	1.67	0.0E+00	4557690	NT	Homo sapiens fibulin 1 (Marfan syndrome) (FBN1) mRNA
3180	8196	13219	0.98	0.0E+00	4507720	NT	Homo sapiens Itln 1 (TN) mRNA
3187	8203	13225	1.67	0.0E+00	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) genes, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
3180	8206	13228	3.59	0.0E+00	AF055084.1	NT	Homo sapiens very large C-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3193	8209	13230	1.14	0.0E+00	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440) mRNA
3193	8209	13231	1.14	0.0E+00	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440) mRNA
3201	10045	13238	2.89	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1) mRNA
3201	10045	13239	2.89	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1) mRNA
3218	8233	13254	2.91	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein P270 mRNA, partial cds

Page 197 of 209
 Table 4
 Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3219	8234	12325	-	1.97 0.0E+00	8823624 NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA	
3231	8246	13268	-	1.1 0.0E+00	7657038 NT	Homo sapiens death receptor 8 (DR8), mRNA	
3250	8263	13284	6	0.0E+00 AI589284.1	EST_HUMAN P25121	60S RIBOSOMAL PROTEIN L11 :contains Alu repetitive element; Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6	Ir63698_X2 NCI_CGAP_Pen 1 Homo sapiens cDNA clone IMAGE:2222535 3' similar to SW:RL11_RAT
3257	8270	13292	2.09	0.0E+00 AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6	
3267	8270	13293	2.09	0.0E+00 AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6	
3268	8271	13294	0.78 0.0E+00	7657213 NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA		
3258	8271	13285	0.78 0.0E+00	7657213 NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA		
3261	8274	13297	1.16 0.0E+00	4502582 NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8), mRNA		
3281	8274	13288	1.16 0.0E+00	4502582 NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8), mRNA		
3264	8277	13300	11.21 0.0E+00	AF111183.1 NT	Homo sapiens Pyrin (MEFV) gene, complete cds		
3268	8279	13302	1.25 0.0E+00	AB040840.1 NT	Homo sapiens mRNA for KIAA1507, protein, partial cds		
3279	8281	13316	0.86 0.0E+00	AI832569.1 EST_HUMAN	AI832569.1 ZINC FINGER PROTEIN :		wb10f04_x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2305278 3' similar to TR:Q91928 Q91928
3312	8323	13348	3.08 0.0E+00	AU123884.1 EST_HUMAN	AU123884.1 AU123664 NT2RM2000735 5'		
3319	8328	13349	0.95 0.0E+00	7383436 NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA		
3319	8329	13350	0.85 0.0E+00	7383436 NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA		
3322	8332	13352	1.91 0.0E+00	7706239 NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA		
3323	8333	13353	1.03 0.0E+00	AF211189.1 NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1a Isoform (CACNA1I) mRNA, complete cds		
3327	8337	13357	0.97 0.0E+00	AW867015.1 EST_HUMAN	MR1-SN0033-100400-001-008 SN0033 Homo sapiens cDNA		
3340	8349	13366	1.39 0.0E+00	7682401 NT	Homo sapiens KIAA0852 protein (KIAA0852), mRNA		
3340	8349	13367	1.39 0.0E+00	7682401 NT	Homo sapiens KIAA0852 protein (KIAA0852), mRNA		
3341	8350	13368	1.13 0.0E+00	4502598 NT	Homo sapiens headed filament structural protein 1, filensin (GFSP1) mRNA		
3343	8352	13369	2.13 0.0E+00	5603067 NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA		
3352	8352	13228	1.45 0.0E+00	AF110763.1 NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds		
3357	8365	13382	2.22 0.0E+00	7657038 NT	Homo sapiens death receptor 6 (DR6), mRNA		
3358	8366	13383	1.37 0.0E+00	6453865 NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA		
3358	8366	13384	1.37 0.0E+00	5453985 NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA		
3361	8369	13388	0.66 0.0E+00	AJ277276.1 NT	Homo sapiens mRNA for reper-2 (repa gene)		
3361	8369	13389	0.66 0.0E+00	AJ277276.1 NT	Homo sapiens mRNA for reper-2 (repa gene)		
3362	8370	13390	4.76 0.0E+00	K02380.1 NT	Bacteriophage P1 replication region including repA, repA, and repB genes and incA, incB, and incC	Incompatibility determinants	

Table 4

Single Exon Probes Expressed In HBL100 Cells

Probe Seq ID NO:	Exon Seq ID NO:	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3364	8372	13392	1.12	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
3367	8375	13395	1.1	0.0E+00	4657746	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET) mRNA
3373	8381	13400	4.09	0.0E+00	AI935158.1	EST_HUMAN	WP_14d10_x1_NCI_CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2464819 3'-similar to TR:073634 O73634
3373	8381	13401	4.09	0.0E+00	AI935159.1	EST_HUMAN	WP_14d10_x1_NCI_CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2464819 3'-similar to TR:073634 O73634
3377	8385	13406	1.61	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (OREF1)
3385	8383	13416	6.22	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3385	8393	13417	5.22	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3391	8389	13425	1.11	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
3397	8405	13431	6.63	0.0E+00	U43293.1	NT	Human MDS1A (AML1/MDS1 fusion) mRNA, partial cds
3401	8410	13435	0.89	0.0E+00	95568718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3401	8410	13436	0.99	0.0E+00	95568718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3405	8414	13441	2.65	0.0E+00	AF05452.1	NT	Human transcriptional regulatory protein p54 mRNA, complete cds
3405	8414	13442	2.65	0.0E+00	AF05452.1	NT	Human transcriptional regulatory protein p54 mRNA, complete cds
3413	8422	13451	1.04	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21, unknown mRNA
3423	8431	13457	1.44	0.0E+00	4508028	NT	Homo sapiens zinc finger protein 45 (a Kruppel-associated box (KRB) domain polypeptide) (ZNF45) mRNA
3426	8434	13459	2.04	0.0E+00	BE304791.1	EST_HUMAN	M143853-1 NIH 3T3 mRNA clone IMAGE:3051373 5'
3426	8434	13460	2.04	0.0E+00	BE304791.1	EST_HUMAN	M143853-7 NIH 3T3 mRNA clone IMAGE:3051373 5'
3429	8437	13463	1.11	0.0E+00	4926785	NT	Homo sapiens potassium voltage-gated channel, 1st-related family, member 2 (KCNE2) mRNA
3431	8439	13466	1.05	0.0E+00	O14867	SWISSPROT	TRANSSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3436	8444	13470	0.83	0.0E+00	AI384007.1	EST_HUMAN	1635912_x1_Searcs_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3'-similar to TR:000498
3439	8447	13473	1.05	0.0E+00	M109787.1	NT	Human endogenous retroviral DNA (-1), complete retroviral segment
3454	8462	13489	1.63	0.0E+00	AB032979.1	NT	601142853-7 NIH 3T3 mRNA clone IMAGE:3051373 5'
3454	8462	13490	1.53	0.0E+00	AB032979.1	NT	Homo sapiens potassium voltage-gated channel, 1st-related family, member 2 (KCNE2) mRNA
3463	8471	13498	0.86	0.0E+00	AV701869.1	EST_HUMAN	601142853-7 NIH 3T3 mRNA clone IMAGE:3051373 5'
3465	8473	13497	1.08	0.0E+00	4506884	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3467	8475		2.85	0.0E+00	AF0781868.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3476	8483	13503	1.11	0.0E+00	AL133204.1	NT	Novel human gene mapping to chromosome X
3477	8485	13504	0.77	0.0E+00	AB040809.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3485	8483	13510	1.54	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
3493	8501	13515	0.94	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila) like 1 (SALL1), mRNA

Page 199 of 209
 Table 4
 Single Exon Probes Expressed in HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3493	8501	13516	0.94	0.0E+00	6397248	NT	Hom sapiens sat (Drosophila)-like 1 (SALL1), mRNA cx77611_X1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1662356 3' similar to WP:T1884.4
3494	8502		1.7	0.0E+00	AI081907.1	EST_HUMAN	CE:13742;
3496	8504	13519	1.01	0.0E+00	6325463	NT	Hom sapiens butyrophilin, subfamily 3, member A3 (BTNSA3), mRNA QVO-CT0225-230300-169-e01 CT0225
3500	8508		4.62	0.0E+00	AW852217.1	EST_HUMAN	Hom sapiens cDNA clone IMAGE:1662356 3' similar to WP:T1884.4
3504	8512	13527	1.42	0.0E+00	4504284	NT	Hom sapiens histone family, member K (H3FK), mRNA cp94h06_s1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:4248596 5'
3508	8516		6.88	0.0E+00	AF116846.1	NT	Hom sapiens gamma-glutamylcysteine synthetase (GCLC) gene, partial cds 80208583F-1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4248596 5'
3509	8517	13528	7.78	0.0E+00	BF678383.1	EST_HUMAN	Hom sapiens histone H3 histone family, member K (H3FK), mRNA cp94h06_s1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1594043 3' similar to contains MER29_b2
3513	8521		1.01	0.0E+00	AA988715.1	EST_HUMAN	MER29 repetitive element.
3522	8528	13539	1.4	0.0E+00	AW897977.1	EST_HUMAN	QVO-DT0047-170206-1-123-901 DT0047 Homo sapiens cDNA clone IMAGE:4283845 5'
3535	8541	13547	0.98	0.0E+00	BF672054.1	EST_HUMAN	602152486F-1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283845 5'
3535	8541	13548	0.98	0.0E+00	BF672054.1	EST_HUMAN	602152486F-1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283845 5'
3538	8542		1.13	0.0E+00	48268687	NT	Hom sapiens retinoblastoma-binding protein 2 (RB1BP2), mRNA hi84801_X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28780243
3538	8544	13550	0.75	0.0E+00	AW864093.1	EST_HUMAN	Hi84801_X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28780243
3538	8544	13551	0.75	0.0E+00	AW864093.1	EST_HUMAN	Hi84801_X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28780243
3541	8547	13555	0.72	0.0E+00	7662319	NT	Hom sapiens KIAA0806 gene product (KIAA0806), mRNA hi84801_X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28780243
3546	8553	13560	2.09	0.0E+00	4557752	NT	Hom sapiens midline 1 (Optiz/BBB syndrome) (MID1) mRNA hi84801_X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28780243
3546	8553	13561	2.09	0.0E+00	4557752	NT	Hom sapiens midline 1 (Optiz/BBB syndrome) (MID1) mRNA hi84801_X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28780243
3562	8569	13574	2.29	0.0E+00	DB7327.1	NT	Hom sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds hi84801_X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28780243
3566	8573		14.47	0.0E+00	7663491	NT	Hom sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA hi84801_X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28780243
3563	8590	13594	3.35	0.0E+00	AB028542.1	NT	Hom sapiens WAVE2 mRNA for WASP-family protein, complete cds hi84801_X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28780243
3564	8591	13595	1.92	0.0E+00	AB007868.2	NT	Hom sapiens mRNA for KIAA0408 protein, partial cds hi84801_X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28780243
3566	8593	13596	4.2	0.0E+00	AF124250.1	NT	Hom sapiens SH2-containing protein Nsp2 mRNA, complete cds hi84801_X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28780243
3568	8593	13597	4.2	0.0E+00	AF124250.1	NT	Hom sapiens SH2-containing protein Nsp2 mRNA, complete cds hi84801_X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:28780243
3592	8599	13605	1.04	0.0E+00	AA852743.1	EST_HUMAN	NHTBCee15g08r1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCee15g09
3592	8599	13608	1.04	0.0E+00	AA852743.1	EST_HUMAN	NHTBCee15g08r1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCee15g09
3595	8602	13608	1.83	0.0E+00	AL163204.2	NT	Hom sapiens chromosome 21 segment 1S21C004
3595	8602	13609	1.83	0.0E+00	AL163204.2	NT	Hom sapiens chromosome 21 segment 1S21C004
3598	8603	13610	0.93	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds Human mRNA for KIAA0333 gene, partial cds
3598	8603	13611	0.83	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds Human mRNA for KIAA0333 gene, partial cds
3600	8603	13614	1.43	0.0E+00	AW851714.1	EST_HUMAN	IMR2-CT0222-231058-005-e05 CT0222 Homo sapiens cDNA

Page 200 of 209

Table 4
Single Exon Probes Expressed in HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3601	8608	13616	1.91	0.0E+00	5729828	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3603	8810	13618	1.09	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0786 protein, partial cds
3605	86112	13620	1	0.0E+00	O14987	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3607	86114	13622	0.83	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0810 protein, partial cds
3607	86114	13623	0.83	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0810 protein, partial cds
3618	86225	13632	1.01	0.0E+00	5729733	NT	Homo sapiens activator of S phase kinase (ASK) mRNA
3618	86225	13633	1.01	0.0E+00	5729733	NT	Homo sapiens activator of S phase kinase (ASK) mRNA
3623	86330	13635	4.46	0.0E+00	AW288134.1	EST_HUMAN	UI-H-BW0-ajs-e-12-0-U1-s1NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3623	86330	13636	4.46	0.0E+00	AW288134.1	EST_HUMAN	UI-H-BW0-ajs-e-12-0-U1-s1NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3645	86551	13657	1.21	0.0E+00	AB004630.1	NT	Human gene for Type XIX collagen 6 chain, exon 6
3646	86552	13658	0.9	0.0E+00	AA463659.1	EST_HUMAN	ba0601_r1 Soares Nih-HMPu_S1 Homo sapiens cDNA clone IMAGE:812496 5' similar to SW_KRB4_SHEEP_P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4. [1];
3650	86556	13662	1.09	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
3653	86559	13664	4.19	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3674	8879	13682	7.89	0.0E+00	7682183	NT	Homo sapiens KIAA0589 gene product (KIAA0589), mRNA
3677	86882	13685	76.43	0.0E+00	4508178	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
3683	86887	13689	1.39	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythrolestosis virus E26 oncogene related (ERG), mRNA
3683	86887	13690	1.39	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythrolestosis virus E26 oncogene related (ERG), mRNA
3728	8733		0.98	0.0E+00	AF195656.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3730	8734	13731	2.82	0.0E+00	AF179732.1	NT	Pan troglodytes olfactory receptor (PTR208) gene, partial cds
3733	8737	13735	2.36	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3733	8737	13736	2.36	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3734	8738	13737	1.16	0.0E+00	AF020091.1	NT	Homo sapiens smooth muscle myosin heavy chain SM1 mRNA, alternatively spliced, Partial cds
3738	8742	13742	1.16	0.0E+00	4759011	NT	Homo sapiens RAB9, RAS oncogene family (RAB9), mRNA
3741	8745	13745	1.16	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGO71) gene, partial cds
3741	8745	13746	1.16	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGO71) gene, partial cds
3742	8746	13147	1.18	0.0E+00	A1377698.1	EST_HUMAN	le62f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3'
3743	8747		1.17	0.0E+00	AF152498.1	NT	Homo sapiens protoactherin beta 3 (PCDH-beta3) mRNA, complete cds
3744	8748	13748	1.26	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DP1) (DSP) mRNA
3747	8751	13750	36.36	0.0E+00	S78885.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, complete cds
3749	8753	13752	2.74	0.0E+00	7710148	NT	Homo sapiens methyl CPG binding protein 2 (MECP2), mRNA
3750	8754	13753	1.32	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3752	8756	13754	1.1	0.0E+00	AF0886801.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds

Page 201 of 209
 Table 4
 Single Exon Probes Expressed in HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3752	8768	13765	1.1	0.0E+00	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3753	8767	13759	1.03	0.0E+00	4504534	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1D (HTR1D) mRNA
3759	8762	13762	0.81	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5) mRNA
3764	8767	13770	7.3	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXorf5) mRNA
3764	8767	13771	7.3	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXorf5) mRNA
3766	8768	13774	4.16	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3767	8770	13775	1.26	0.0E+00	AF114488.1	NT	Homo sapiens intersecin short isoform (ITS) mRNA, complete cds
3770	8773	13777	1.15	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (Kcnb1) mRNA
3773	8776	13780	2.04	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129) mRNA
							Homo sapiens NC_ CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR:O4340
3784	8787	13781	2.48	0.0E+00	AI864727.1	EST_HUMAN	Wk01f01_X1 NC_ CGAP_Lym12 Homo sapiens cDNA clone PTR7 repetitive element :
3787	8780	13785	20.27	0.0E+00	4506742	NT	Homo sapiens ribosomal protein S8 (RPS8) mRNA
3788	8792	13787	1.47	0.0E+00	AL040328.1	EST_HUMAN	DKFZp434N0413_r1_434 (synonym: hsc3) Homo sapiens cDNA clone DKFZp434N0413 5'
3789	8797	13803	0.97	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1) mRNA
3794	8797	13804	0.97	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1) mRNA
3794	8797	13804	0.97	0.0E+00	6005887	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
3795	8798	13805	1.95	0.0E+00	4504138	NT	Homo sapiens melanoma antigen, family B_1 (MAGEB1) mRNA
3796	8798	13806	1.87	0.0E+00	4505078	NT	Homo sapiens HBp17 heparin-binding and FGF-binding protein gene, complete cds
3800	8803	13808	0.87	0.0E+00	AF149442.1	NT	Homo sapiens tyrosine receptor kinase receptor 3 (RYR3) mRNA
3808	8811	13817	1.69	0.0E+00	4508758	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
3812	8816	13821	2.31	0.0E+00	4585642	NT	Homo sapiens F-box protein FBXb (FBX3B) mRNA, partial cds
3824	8826	13833	1.81	0.0E+00	AF129533.1	NT	Homo sapiens cDNA clone IMAGE:36038800 5'
3828	8831	13838	3.61	0.0E+00	BE378502.1	EST_HUMAN	601236986F1_NIH_MGC_44 Homo sapiens cDNA clone IMAGE:36038800 5'
3836	8838	13844	2.13	0.0E+00	AW680740.1	EST_HUMAN	PM3-LT0031-100100-003-h09 LT0031 Homo sapiens cDNA clone IMAGE:3537774 5'
3837	8839	13845	1.01	0.0E+00	BE26498.1	EST_HUMAN	601193827F1_NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537774 5'
3837	8839	13846	1.01	0.0E+00	BE28498.1	EST_HUMAN	Novel human gene mapping to chromosome 20
3883	8889	13872	4.2	0.0E+00	AF116186.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3888	8889	13873	4.2	0.0E+00	AF116185.1	NT	Human MHC class II lymphocyte antigen DPw4-bebe-2 pseudogene, exon 2
3879	8879		4.42	0.0E+00	M23910.1	NT	Homo sapiens chromosome 21 segment HS21C103
3881	8882		5.98	0.0E+00	AL168303.2	NT	Homo sapiens chromosome 21 segment HS21C084
3887	8886	13887	0.83	0.0E+00	AL118494.1	NT	Homo sapiens chromosome 21 segment HS21C068
3891	8891	13889	2.84	0.0E+00	AL163268.2	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
3911	8911	13897	2.2	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA

Page 202 of 209
 Table 4
 Single Exon Probes Expressed In HBL100

Probe Seq ID NO:	Exon Seq ID NO:	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							h155g08_x1_NCL_CGAP_QC8 Homo sapiens cDNA clone IMAGE:2244734 3' similar to TR:080309_080309
3914	8914		1.34	0.0E+00	AJ857076.1	EST_HUMAN	KIAA0563 PROTEIN :
3916	8916	13910	2.58	0.0E+00	U08266.1	NT	Human zinc finger protein 2NF133
3933	8932	13925	12.81	0.0E+00	AB015610.1	NT	Chlorocebous aethiops mRNA for ribosomal protein S4X, complete cds
3941	8939		3.58	0.0E+00	AJ238617.1	NT	Homo sapiens mRNA for KIAA0318 protein, partial cds
3951	8949	13938	1.39	0.0E+00	AB002314.2	NT	Homo sapiens mRNA for KIAA0318 protein, partial cds
3952	8950	13939	1.78	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
3953	8951	13940	2.58	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for repa-2 (repa gene)
3953	8951	13941	2.58	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for repa-2 (repa gene)
3961	8959	13948	14.88	0.0E+00	50320226	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
3961	8959	13949	14.88	0.0E+00	50320226	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
3969	8968	13987	1.91	0.0E+00	4503914	NT	Homophosphorylaminomimidazole synthetase (SART) mRNA
3973	8971	13959	4.78	0.0E+00	4985306	NT	Homo sapiens G protein-coupled receptor 21 (GPR21) mRNA
3974	8972	13960	1.41	0.0E+00	AB016625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
3977	8975	13961	0.8	0.0E+00	4788807	NT	Homo sapiens GTPase activating protein-like (NGAP) mRNA
3978	8976	13962	7.12	0.0E+00	11419287	NT	Homo sapiens MP (Inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
3979	8977	13963	3.69	0.0E+00	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
							z555e011 Socres retina N2b4HR Homo sapiens cDNA clone IMAGE:352820 5' similar to contains Alu repetitive element.
3980	8978		0.98	0.0E+00	AA018975.1	EST_HUMAN	
3986	8984	13970	3.76	0.0E+00	AF165537.1	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
3991	10050	13974	1.98	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
3995	6121	11150	1.11	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
3995	6121	11151	1.11	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4000	8996	13984	1.04	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
4000	8996	13985	1.04	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
4003	8999	13987	1.39	0.0E+00	892239	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
4003	8999	13988	1.39	0.0E+00	892239	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4008	9002	13989	1.03	0.0E+00	AB020702.1	NT	Homo sapiens mRNA for KIAA0895, protein, partial cds
4012	9008	13997	6.13	0.0E+00	AJ82587.1	EST_HUMAN	wn04d04_x1_NCI_CGAP_QC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4012	9008	13998	6.13	0.0E+00	AJ82587.1	EST_HUMAN	wn04d04_x1_NCI_CGAP_QC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4014	9010	14000	2.24	0.0E+00	BE18486.1	EST_HUMAN	MR1-HT0707-100500-001-002 HT0707 Homo sapiens cDNA
4014	9010	14001	2.24	0.0E+00	BE18486.1	EST_HUMAN	MR1-HT0707-100500-001-002 HT0707 Homo sapiens cDNA
4018	9014		10.6	0.0E+00	BE274217.1	EST_HUMAN	60112077SF1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2897690 5'

Page 203 of 209
Table 4
Single Exon Probes Expressed in HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							Top Hit	Descriptor
4024	8020	140007	1.02	0.0E+00	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine->gamma-glutamyltransferase) (TGM3)	mRNA
4025	8021	140008	2.26	0.0E+00	5728725	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3)	mRNA
4032	8028	14021	6.78	0.0E+00	AW875598.1	EST_HUMAN	Homo sapiens nuclear receptor coactivator 3 (NCOA3)	mRNA
4037	8033	140201	0.85	0.0E+00	AW408798.1	EST_HUMAN	ba5f04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900095 3' similar to SW:THI2_BOVIN	mRNA
4039	8035	140224	1.61	0.0E+00	8922468	NT	UI-HF-BM0-adx-c-02-0-11.1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3063147 5'	mRNA
4039	8035	140225	1.51	0.0E+00	8922468	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA	mRNA
4048	8044		2.18	0.0E+00	5174632	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA	mRNA
4068	8082	14049	8.89	0.0E+00	AA401438.1	EST_HUMAN	zu88h07.s1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains_Alu repetitive element	mRNA
4068	8082	14050	9.69	0.0E+00	AA401438.1	EST_HUMAN	zu88h07.s1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains_Alu repetitive element	mRNA
4072	8066	14056	1.32	0.0E+00	AF157478.1	NT	zu88h07.s1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains_Alu repetitive element	mRNA
4085	8079	14068	0.94	0.0E+00	4507720	NT	Homo sapiens tRNA	mRNA
4085	8079	14089	0.94	0.0E+00	4507720	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3)mRNA, complete cds	mRNA
4087	8081	14072	1.45	0.0E+00	7862125	NT	Homo sapiens tRNA	mRNA
4101	8085	14079	1.28	0.0E+00	4758189	NT	Homo sapiens desmoplakin (DPI), (DPII) mRNA	mRNA
4101	8085	14080	1.28	0.0E+00	4758189	NT	Homo sapiens desmoplakin (DPI), (DPII) mRNA	mRNA
4109	9103		0.71	0.0E+00	AL163303.2	NT	Homo sapiens cholinesterase 21 segment HS21C03	mRNA
4135	9130	14113	1.98	0.0E+00	AJ003145.1	NT	Homo sapiens mRNA for olfactory receptor protein, Pseudogene	mRNA
4151	9148	14130	2.21	0.0E+00	J02610.1	NT	Human apolipoprotein B-100 mRNA, complete cds	mRNA
4164	9159	14146	0.86	0.0E+00	AW86689.1	EST_HUMAN	PM2-DT023-080300-004-010 D70623 Homo sapiens cDNA	mRNA
4171	9168	14153	4.94	0.0E+00	AF174590.1	NT	Homo sapiens F_box protein Fb14 (FB14) mRNA, partial cds	mRNA
4177	9171		3.4	0.0E+00	AI18944.1	EST_HUMAN	qd23f06.x1 Soares, placenta_Bio9weeks_2NbHP80c6V Homo sapiens cDNA clone IMAGE:1724579 3'	mRNA
4180	9173		5.07	0.0E+00	U14520.1	NT	similar to contains MER20.b2 MER20 repetitive element	mRNA
4183	9176	14160	0.82	0.0E+00	6174574	NT	Homo sapiens myeloid/sympathetic or mixed-lineage leukemia (tritoxa) homolog; translocated to 4 (MLLT4) mRNA	mRNA
4198	9181	14173	1.19	0.0E+00	6583384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA	mRNA
4198	9181	14174	1.19	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA	mRNA
4205	9188	14180	1.28	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds	mRNA
4205	9188	14181	1.28	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds	mRNA

Page 204 of 209
 Table 4
 Single Exon Probes Expressed In HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4215	9208	14187	10.08	0.0E+00	6912281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR) mRNA
4235	9229		1.05	0.0E+00	AF153047.2	NT	Homo sapiens gap junction protein connexin-38 (CX38) gene, complete cds
4245	9239	14222	5.12	0.0E+00	L14681.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4249	9243	14227	4.71	0.0E+00	Z80780.1	NT	H.sapiens H2af/h gene
4249	9243	14228	4.71	0.0E+00	Z80780.1	NT	H.sapiens H2af/h gene
4250	9244	14229	1.5	0.0E+00	AW166833.1	EST_HUMAN	x068e10.x1 NC_ CGAP_J44 Homo sapiens cDNA clone IMAGE:2633514 3' similar to TR:PF97385 PF97385
4250	9250	14235	2.08	0.0E+00	X60483.1	NT	ZINC FINGER PROTEIN 64
4256	9250	14236	2.06	0.0E+00	X60483.1	NT	H.sapiens H4d gene for H4 histone
4266	9264	14242	11.18	0.0E+00	7662091	NT	H.sapiens H4d gene for H4 histone
4261	9264	14243	11.18	0.0E+00	7662091	NT	Homo sapiens KIAA03590 gene product (KIAA03590) mRNA
4261	9264	14243	11.18	0.0E+00	7662091	NT	Homo sapiens KIAA03590 gene product (KIAA03590) mRNA
4274	9267	14258	11.95	0.0E+00	4885428	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4) mRNA
4275	9268	14259	1.08	0.0E+00	AJ271756.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4276	9269		0.98	0.0E+00	AL163207.2	NT	Homo sapiens chromosome 21; segment 1-521C007
4309	9301	14288	1.08	0.0E+00	7018456	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR) mRNA
4320	9312		6.33	0.0E+00	AF185953.1	NT	Homo sapiens membrane-bound meropeptidase P (XNPEP2) gene, complete cds
4325	9317	14289	2.86	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4325	9317	14300	2.86	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4330	9321	14306	0.81	0.0E+00	W28178.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4330	9321	14307	0.81	0.0E+00	W26179.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4344	9335		2.03	0.0E+00	AF200629.1	NT	Homo sapiens HPS1 gene, Intron 5
4362	9353		0.76	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
4372	9364	14344	2.57	0.0E+00	AW084864.1	EST_HUMAN	x068e9e10.x1 NC_ CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2689446 3' similar to SW:AHNK_HUMAN
4374	10052		1.15	0.0E+00	8051619	NT	Q086666 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK; Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4375	9366	14346	0.81	0.0E+00	AF016050.1	NT	Homo sapiens vascular endothelial cell growth factor 165 receptor/neuropilin (VEGF165) mRNA, complete cds
4378	9369		7.59	0.0E+00	AL163207.2	NT	Homo sapiens chromosome 21; segment 1-521C007
4380	9371	14350	1.24	0.0E+00	AW381570.1	EST_HUMAN	PMI-H70305-101198-002-d03 H70305 Homo sapiens cDNA
4386	9377	14357	1.18	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4386	9377	14358	1.18	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4388	9379	14360	1.24	0.0E+00	4755467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4389	9380	14361	3.1	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNKH) mRNA, complete cds

Page 205 of 209
 Table 4
 Single Exon Probes Expressed in HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4398	9389	14372	1.05	0.0E+00	S78584.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNE6/BLR1) gene, exon
4399	9390	14373	1.06	0.0E+00	AF111163.1	NT	Homo sapiens Pyrin (MEFV) gene, complete cds
4399	9390	14374	1.06	0.0E+00	AF111163.1	NT	Homo sapiens Pyrin (MEFV) gene, complete cds
4409	10053	14384	3.16	0.0E+00	6005973	NT	Homo sapiens Zinc finger protein 195 (ZNF195), mRNA
4413	9403	14388	5.97	0.0E+00	AF208181.1	NT	Homo sapiens synaptosomal precursor, mRNA, complete cds
4418	9408	14385	1.83	0.0E+00	AF162337.1	NT	Homo sapiens protocadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4421	9411	14389	1.07	0.0E+00	6454175	NT	Homo sapiens Zinc finger protein 211 (ZNF211), mRNA
4431	9421	14407	50.75	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4438	9428	14412	1.01	0.0E+00	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4442	9432	14416	1.5	0.0E+00	4503098	NT	Homo sapiens chondroitin sulphate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4446	9436	14420	1.11	0.0E+00	4502556	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CaMKIV) mRNA
4449	9439		1.16	0.0E+00	BE871908.1	EST_HUMAN	601447932F11 NIH_3T3
4452	9442		2.72	0.0E+00	L35485.1	NT	Homo sapiens Kuronate sulphatase (IDS) gene, complete cds
4454	9444	14423	11.71	0.0E+00	7662091	NT	Homo sapiens KIAA0350 gene product (KIAA0350), mRNA
4454	9444	14424	11.71	0.0E+00	7662091	NT	Homo sapiens KIAA0350 gene product (KIAA0350), mRNA
4471	9461	14440	2.89	0.0E+00	AF143314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
4473	9463	14442	10.04	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4473	9463	14443	10.04	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4475	9465	14444	0.8	0.0E+00	AB018338.1	NT	Homo sapiens mRNA for KIAA0705 protein, partial cds
4480	9460		1.45	0.0E+00	AA1174072.1	EST_HUMAN	2p18q8.1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:6098854.3
4492	9482		1.39	0.0E+00	7657410	NT	Homo sapiens odz (odd Oz/zen-m, Drosophila) homolog 1 (ODZ1), mRNA
4494	9484		2.8	0.0E+00	AL163284.2	NT	Homo sapiens HS21C084
4495	9485	14463	1.18	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4496	9486	14464	5.1	0.0E+00	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4497	9487		1.83	0.0E+00	AB0371521.1	NT	Homo sapiens gene for natriuretic protein, partial cds
4499	9489	14485	0.9	0.0E+00	AF198558.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4502	9492	14469	1.33	0.0E+00	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4507	9497	14475	11.33	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4507	9497	14476	11.33	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4508	9508	14477	2.06	0.0E+00	AF1617441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4518	9508	14489	0.84	0.0E+00	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds

Page 206 of 209
 Table 4
 Single Exon Probes Expressed In HBL-100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit No.	Top Hit Database Source	Top Hit Descriptor
4518	9508	14880	0.94	0.0E+00	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4518	9508	14481	0.94	0.0E+00	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4519	9509	14482	1.58	0.0E+00	AB028570.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4519	9509	14483	1.68	0.0E+00	AB028570.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4524	9514	14489	3.45	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), s89, pol and env genes
4530	9520	14507	1.32	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0385-180400-142-105 B10635 Homo sapiens cDNA clone IMAGE:787605 3'
4531	9521	14508	1.01	0.0E+00	AA418246.1	EST_HUMAN	ZB6507_s1 Speces_NiHMPu_S1 Homo sapiens cDNA clone IMAGE:787605 3'
4536	9528		2.02	0.0E+00	AF088641.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4541	9530	14517	2.53	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1398 protein, partial cds
4541	9530	14518	2.63	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1398 protein, partial cds
4542	9531	14519	2.25	0.0E+00	MT4098.1	NT	Human displacement protein (CCAA1) mRNA
4544	9533	14521	2.88	0.0E+00	6463812.1	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4544	9533	14522	2.88	0.0E+00	8453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4549	9537		1.17	0.0E+00	BE278730.1	EST_HUMAN	601165935F-1 NiH_MGC_21 Homo sapiens cDNA clone IMAGE:35056321 5'
4570	9558	14546	1.12	0.0E+00	5729817	NT	Homo sapiens ectropic viral integration site 2B (EV12B), mRNA
4570	9558	14547	1.12	0.0E+00	5729817	NT	Homo sapiens ectropic viral integration site 2B (EV12B), mRNA
4575	9563	14551	5.79	0.0E+00	MB09022.1	NT	Human AHNAK nucleoprotein mRNA, 5' end
4578	9568	14554	2.21	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4578	9568	14555	2.21	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4581	9569	14558	1.86	0.0E+00	AF184110.1	NT	Human NKTR gene, complete cds
4582	9570	14559	0.68	0.0E+00	76624779	NT	Homo sapiens KIAA1084 protein (KIAA1084), mRNA
4583	9571	14560	2.97	0.0E+00	7662181	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4590	9578	14568	1.07	0.0E+00	U07563.1	NT	Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds
4594	9582	14572	1.24	0.0E+00	AL0986857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4599	9587		1.15	0.0E+00	X58487.1	NT	Human CYP2D7AP pseudogene for cytochrome P450 2D7
4615	9600	14588	1.22	0.0E+00	AF026801.1	NT	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-28
4617	9602	14588	1.69	0.0E+00	6677700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4617	9602	14589	1.99	0.0E+00	6677700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4618	9603	14590	0.75	0.0E+00	7016820	NT	Homo sapiens proteinx008 (AD013), mRNA
4618	9603	14591	0.76	0.0E+00	7016820	NT	Homo sapiens proteinx008 (AD013), mRNA
4641	9626	14618	1.66	0.0E+00	AW444837.1	EST_HUMAN	U1-H-B13-8M-2-0-0-1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2733284 3'
4647	9632	14627	1.01	0.0E+00	AF303134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12), mRNA, complete cds

Page 207 of 209
 Table 4
 Single Exon Probes Expressed in HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source.	Top Hit Descriptor
4649	9634		1.44	0.0E+00	AF053242.1	NT	Homo sapiens HSPO24-iso mRNA, complete cds
4688	9873	14655	0.68	0.0E+00	J00191.1	NT	Human MHC class I transplantation antigen (hla) gene
4688	9873	14656	0.68	0.0E+00	J00191.1	NT	Human MHC class I transplantation antigen (hla) gene
4694	9879		6.98	0.0E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4698	9683	14666	2.39	0.0E+00	X87205.1	NT	M. fasciculans mRNA for metalloprotease-like protein, IV
4700	9685	14668	1.77	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Bauren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds
4701	9866	14669	1.47	0.0E+00	AF097418.1	NT	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds
4702	9687	14670	4.25	0.0E+00	4503768	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4704	9689	14672	13.59	0.0E+00	4886048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC) mRNA
4706	9691	14674	2.35	0.0E+00	8922180	NT	Homo sapiens hypothetical protein DKF7p762E1312 (DKF7p762E1312) mRNA
4709	9694	14678	7.7	0.0E+00	8923050	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073) mRNA
4712	8697	14681	2.67	0.0E+00	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187) mRNA
4713	9698	14682	1.91	0.0E+00	M94081.1	NT	Human Tcr-C-Delta gene, exons 1-4; Tcr-V-Delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments, and Tcr-C-alpha gene, exons 1-4
4713	9698	14683	1.91	0.0E+00	M94081.1	NT	Human Tcr-C-Delta gene, exons 1-4; Tcr-V-Delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments, and Tcr-C-alpha gene, exons 1-4
4715	9700	14685	1.8	0.0E+00	X94628.1	NT	H. sapiens Macf-2 gene
4715	9700	14686	1.8	0.0E+00	X94628.1	NT	H. sapiens Macf-2 gene
4718	9703	14689	1.87	0.0E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C050
4727	9712	14697	1.27	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28D (TAF2)
4732	9717	14702	3.92	0.0E+00	X92841.1	NT	H. sapiens MICA gene
4734	9719	14704	1.68	0.0E+00	48865642	NT	Homo sapiens zinc finger protein (KIAA0142) mRNA
4735	9720	14705	1.08	0.0E+00	AB0317884.1	NT	Homo sapiens mRNA for KIAA01443 protein, partial cds
4736	9721	14706	0.92	0.0E+00	AB014533.1	NT	Homo sapiens mRNA for KIAA01633 protein, partial cds
4737	9722	14707	2.29	0.0E+00	6677648	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zik1), mRNA
4738	9723	14708	1.04	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (collected-coll proline-rich) (MGCA6), mRNA
4740	9725	14710	1.45	0.0E+00	4758199	NT	Homo sapiens desmoglein (Dp), (Dp1) (Dp1) mRNA
4744	9728	14716	38.01	0.0E+00	AF055066.1	NT	Homo sapiens opioid receptor, delta 1 (OPRD1) mRNA
4746	9731		2.39	0.0E+00	4605508	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
4747	9732	14718	2.63	0.0E+00	AF091711.1	NT	Homo sapiens collagen type IV alpha 6 (COL4A6) gene for collagen, exon 44 and partial cds
4760	9744	14730	1.02	0.0E+00	D85562.1	NT	Homo sapiens collagen type IV alpha 6 (COL4A6) gene for collagen, exon 44 and partial cds

Page 208 of 209
 Table 4
 Single Exon Probes Expressed in HBL-100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4762	9748	14732	1.98	0.0E+00	4503684	NT	Homo sapiens farnesyI diphosphate synthase (farnesyI pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDPS) mRNA
4764	9748	14735	1.13	0.0E+00	AI249052.1	EST_HUMAN	q968d08_x1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849839 3' similar to SW:ATPN_BOVIN_Q28852_ATP_SYNTHASE_G_CHAIN MITOCHONDRIAL;
4764	9748	14736	1.13	0.0E+00	AI249052.1	EST_HUMAN	q968d08_x1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849839 3' similar to SW:ATPN_BOVIN_Q28852_ATP_SYNTHASE_G_CHAIN MITOCHONDRIAL;
4768	9752		1.07	0.0E+00	AI291128.1	EST_HUMAN	qm15f05_x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881921 3' similar to TR:Q61632_Q61632 EN-2LAC2 FUSION PROTEIN;
4795	9778	14762	1.2	0.0E+00	AI163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4801	9775	14767	1.02	0.0E+00	78662319	NT	Homo sapiens KIAA0808 gene product (KIAA0808) mRNA
4808	9782	14774	0.86	0.0E+00	AA205437.1	EST_HUMAN	zq86b08_s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:846547 3'
4813	9797		6.87	0.0E+00	U14987.1	NT	Human ribosomal protein L21 mRNA, complete cds
4823	9807	14789	1.6	0.0E+00	IM10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
4825	9809		2.99	0.0E+00	BE408883.1	EST_HUMAN	6013031728F_NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 6'
4829	9813	14784	3.55	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DP1, DP11) (DSP) mRNA
4838	9820	14787	2.16	0.0E+00	AB028986.1	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds
4848	9830	14804	2.53	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477) mRNA
4848	9830	14805	2.53	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477) mRNA
4862	9843	14815	1	0.0E+00	AA601246.1	EST_HUMAN	no14g09_s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:EE239140
4862	9843	14816	1	0.0E+00	AA601246.1	EST_HUMAN	E239140 SPALT PROTEIN;
4862	9843		1	0.0E+00	AA601246.1	EST_HUMAN	no14g09_s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:EE239140
4862	9843	14817	1	0.0E+00	AA601246.1	EST_HUMAN	E239140 SPALT PROTEIN;
4864	9844	14818	1.59	0.0E+00	AF161683.1	NT	Homo sapiens HSPC114 mRNA, complete cds
4864	9844	14819	1.59	0.0E+00	AF161683.1	NT	Homo sapiens HSPC114 mRNA, complete cds
4867	9275	10289	0.81	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4870	9849		0.92	0.0E+00	4758225	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
4881	9860	14831	1.28	0.0E+00	AF016705.1	NT	Homo sapiens EB-AP ubiquitin-protein ligase (UBE3A) gene, exon 3
4883	9862	14833	1.27	0.0E+00	U53588.1	NT	Homo sapiens MHC class 1 region
4887	9866		1.11	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4890	9869		27.33	0.0E+00	D506657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
4913	9892	14866	3.61	0.0E+00	X62988.1	NT	Bacillus amyloliquefaciens stacB gene for levansucrase (EC 2.4.1.10)
4927	9904	14892	2.48	0.0E+00	AF272293.1	NT	Homo sapiens gophyrin mRNA, complete cds

Page 209 of 209
 Table 4
 Single Exon Probes Expressed in HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4930	8807	14884	1.13	0.0E+00	5454153	NT	<i>Homo sapiens cyclothilin (USA-CYP) mRNA</i>
4936	8913	14891	0.99	0.0E+00	AA1683268.1	EST_HUMAN	<i>aa32b04.s1 Strategene schizo brain S11 cDNA clone IMAGE:1020387 3'</i>
4951	8928	14896	0.95	0.0E+00	4857352	NT	<i>Homo sapiens PR domain containing 1, with ZNF domain (PRDM1) mRNA</i>
4957	8934	14912	0.72	0.0E+00	Y08032.1	NT	<i>Human endogenous retrovirus-K, LTR U5 and gag gene</i>
4965	8942	14919	0.92	0.0E+00	AF124250.1	NT	<i>Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds</i>
4980	8945	14933	0.92	0.0E+00	7882421	NT	<i>Homo sapiens KIAA0971 protein (KIAA0971), mRNA</i>
4981	8956	14934	0.67	0.0E+00	4826785	NT	<i>Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA</i>
4990	8963	14940	1.07	0.0E+00	AF108830.1	NT	<i>Homo sapiens serine-threonine protein kinase (MNBP) mRNA, complete cds</i>
4990	8963	14941	1.07	0.0E+00	AF108830.1	NT	<i>Homo sapiens serine-threonine protein kinase (MNBP) mRNA, complete cds</i>
6009	8980	14955	1.27	0.0E+00	7657263	NT	<i>Homo sapiens acidic 82 kDa protein mRNA (HSU16552), mRNA</i>
5034	10005	14976	1.17	0.0E+00	4758021	NT	<i>Homo sapiens coagulation factor C (Umulis polyphemus) homology (COCH), mRNA</i>
5049	10020	14989	0.99	0.0E+00	8877700	NT	<i>Homo sapiens G-protein coupled receptor (RE2), mRNA</i>
5049	10020	14990	0.99	0.0E+00	8877700	NT	<i>Homo sapiens G-protein coupled receptor (RE2), mRNA</i>
5053	10024	14993	0.74	0.0E+00	7857336	NT	<i>Homo sapiens mull. (E. coli) homolog 3 (MLH3), mRNA</i>
5058	10037	15004	0.76	0.0E+00	AL044081.1	EST_HUMAN	<i>DKFZp434L2128_1' 434 (synonym: hts3) Homo sapiens cDNA clone DKFZp434L2128 6'</i>

PC IV CO CO 00000000

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human Breast comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 5,074 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
- 15 3. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
- 20 4. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 5,075 - 10,058.
- 25 5. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
- 30 6. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
- 35 7. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 5 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 10 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in 15 that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is 20 selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of 25 single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Breast 30 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 5,074 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human Breast.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 5,075 - 10,058 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Breast which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOS.: 10,059 - 15,009, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Breast.

16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

25

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30 20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

35 21. A single exon nucleic acid probe as claimed in any one of claims 13 - 20, wherein said probe lacks homopolymeric

stretches of A or T.

22. A method of measuring gene expression in a sample derived from human Breast, comprising:

5 contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human Breast; and then measuring the label detectably bound to each probe of
10 said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

15 algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe, wherein said detectably labeled nucleic acids are derived from mRNA from the Breast of said eukaryote, said probe is
20 a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively hybridizable at high stringency.

25 24. A method of assigning exons to a single gene, comprising:

30 identifying a plurality of exons from genomic sequence according to the method of claim 23; and then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,
35 wherein a common pattern of expression of said exons in

said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID Nos: 1 - 10,058 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 10,058.

10 27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 10,059 - 15,009.

1/10

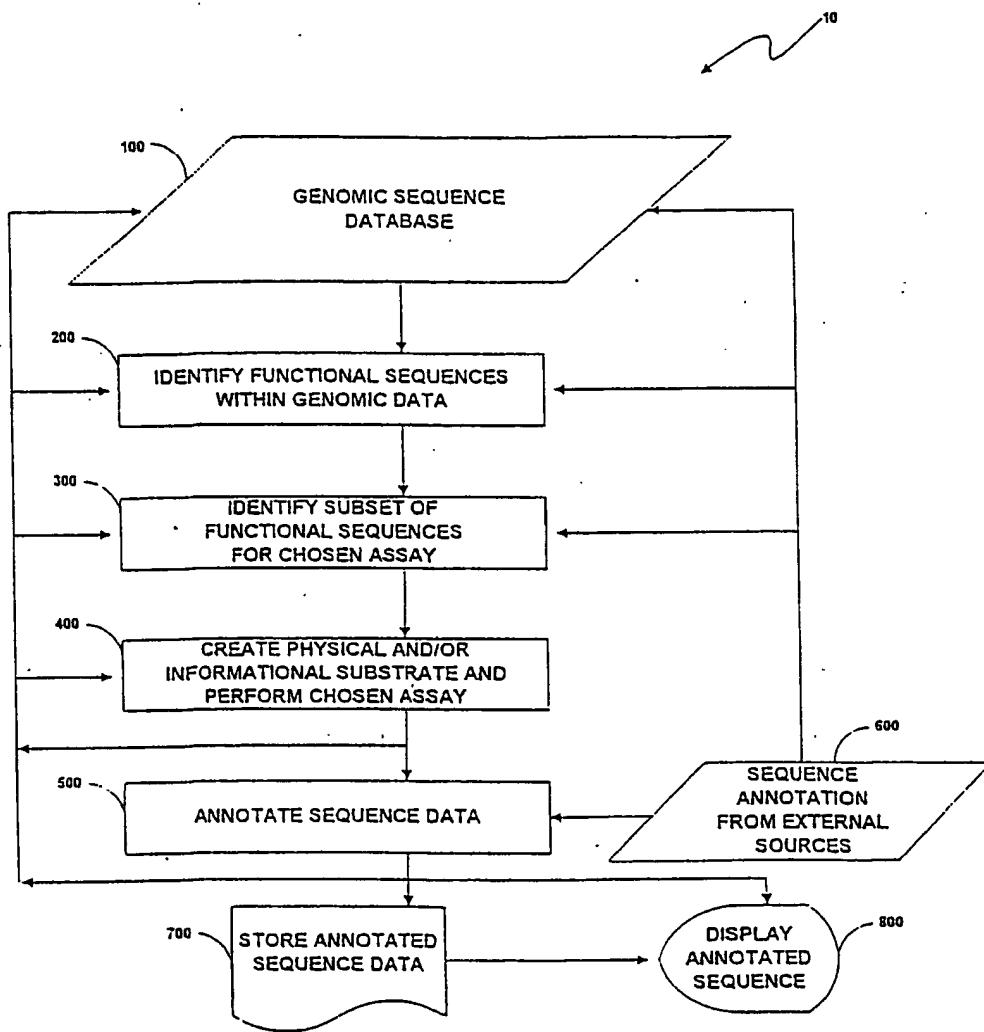


Fig. 1

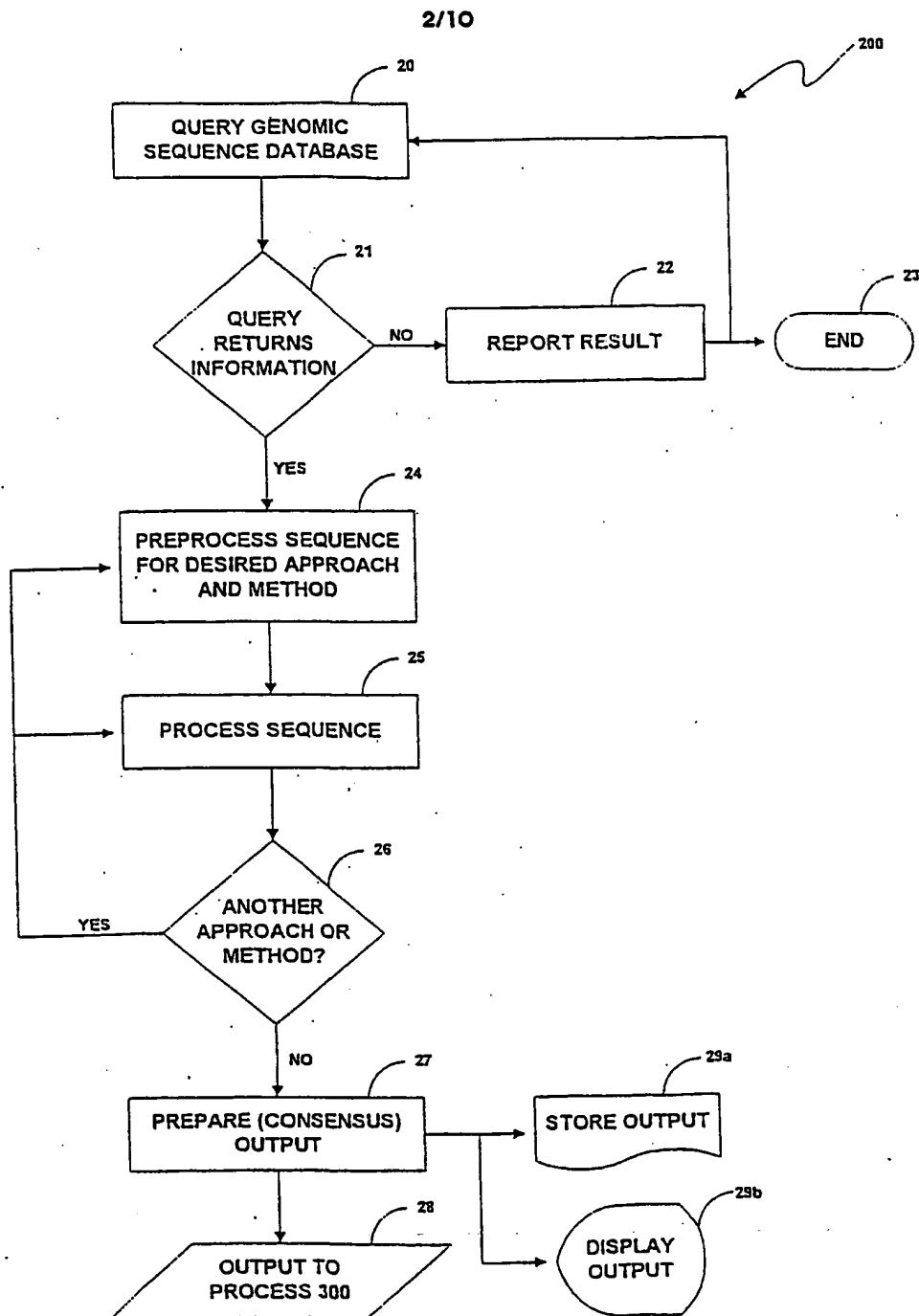


Fig. 2

3/10

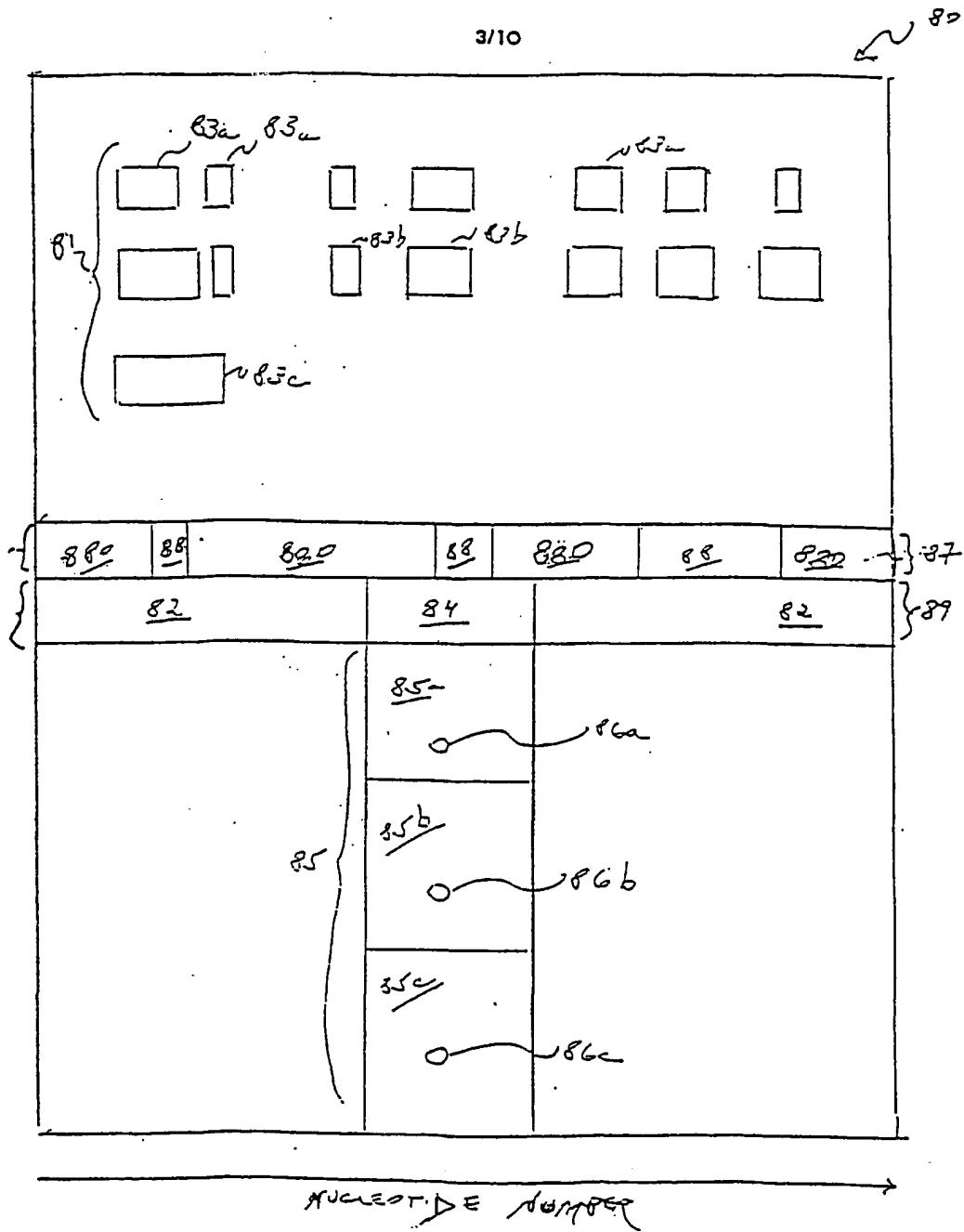


Fig. 3

4/10

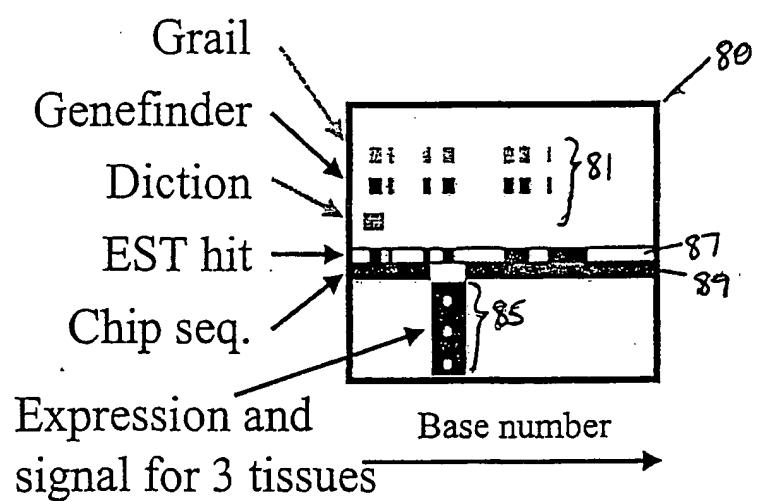


Fig. 4

5/10

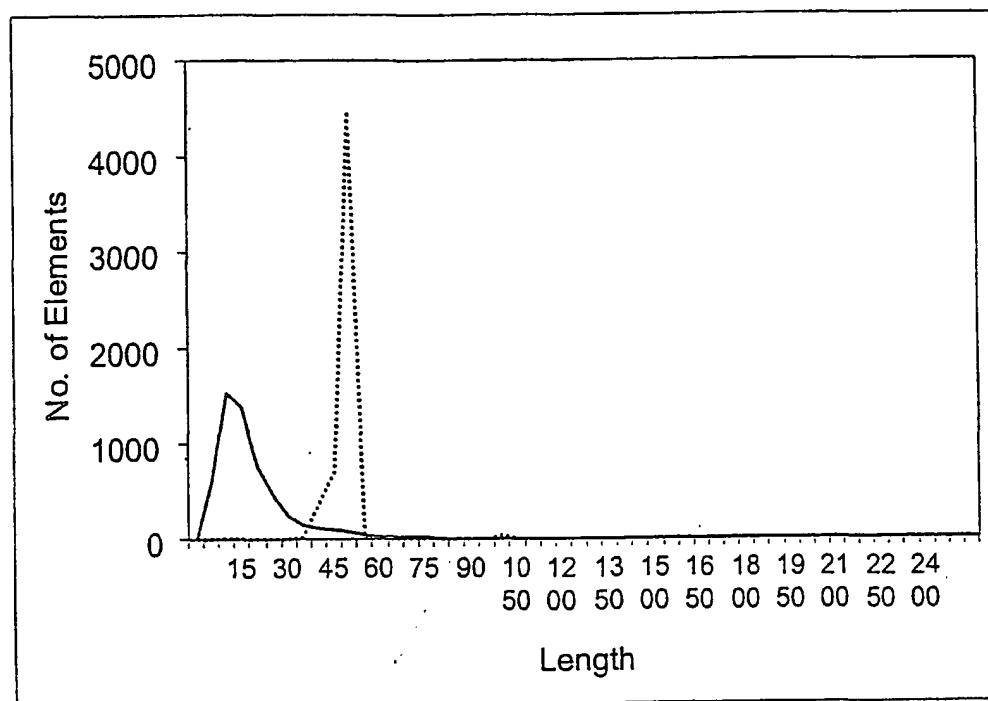


Fig. 5

6/10

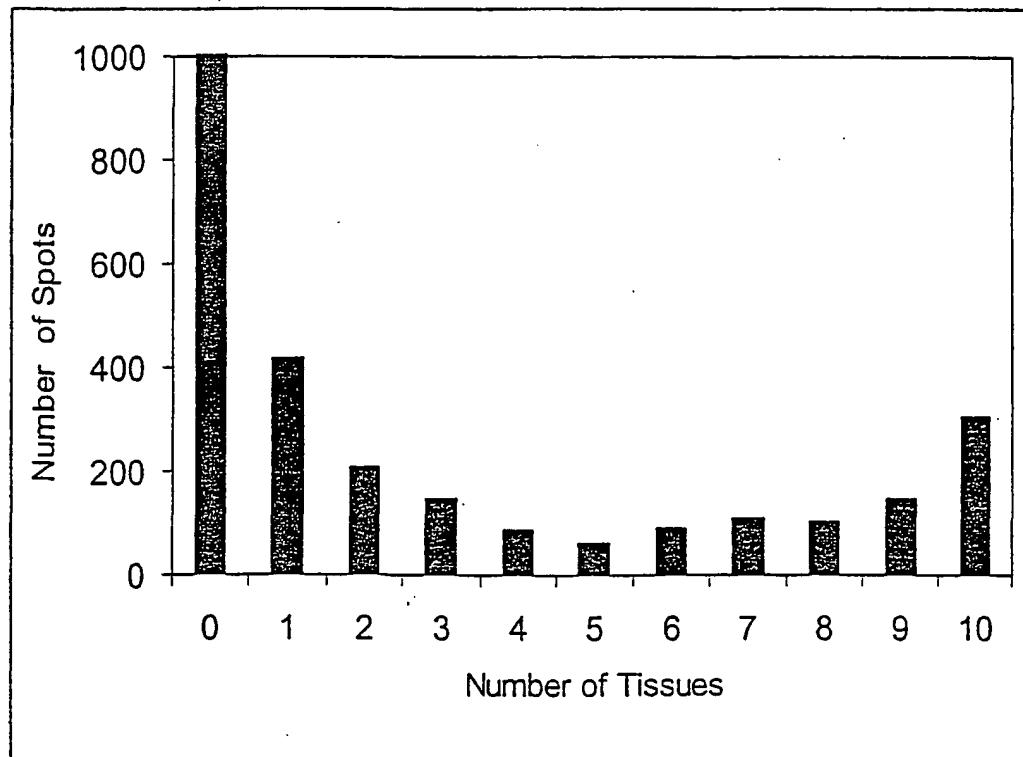


Fig. 6

7/10

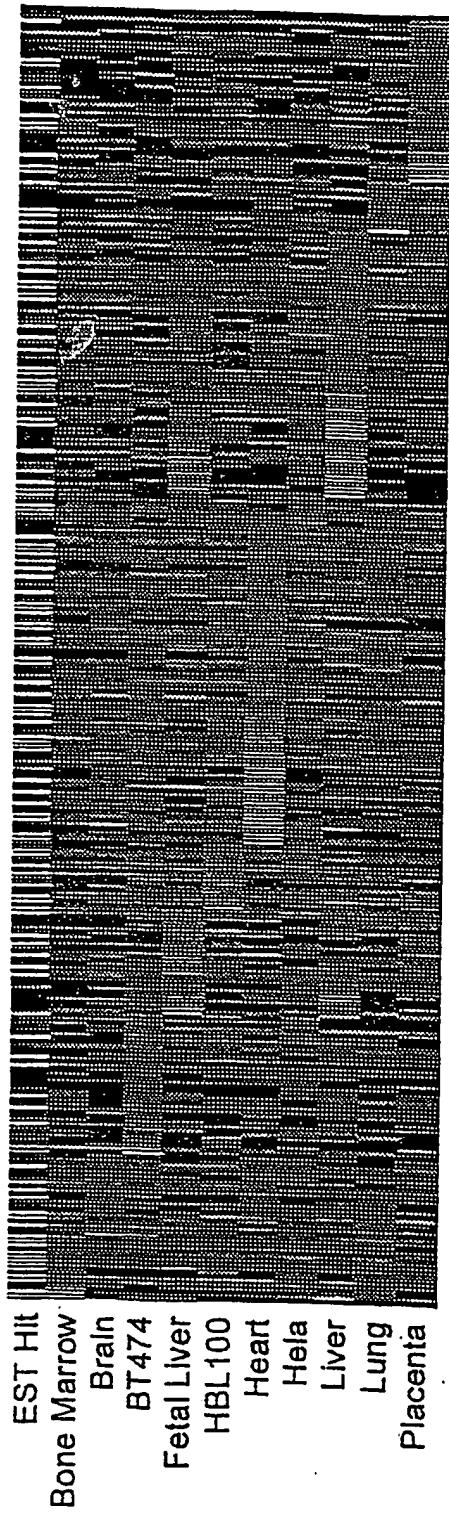


Fig. 7a

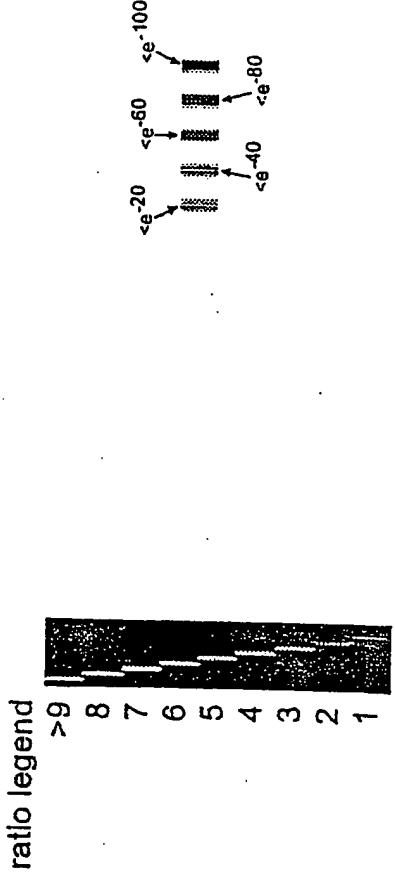


Fig. 7b

Fig. 7c

8/10

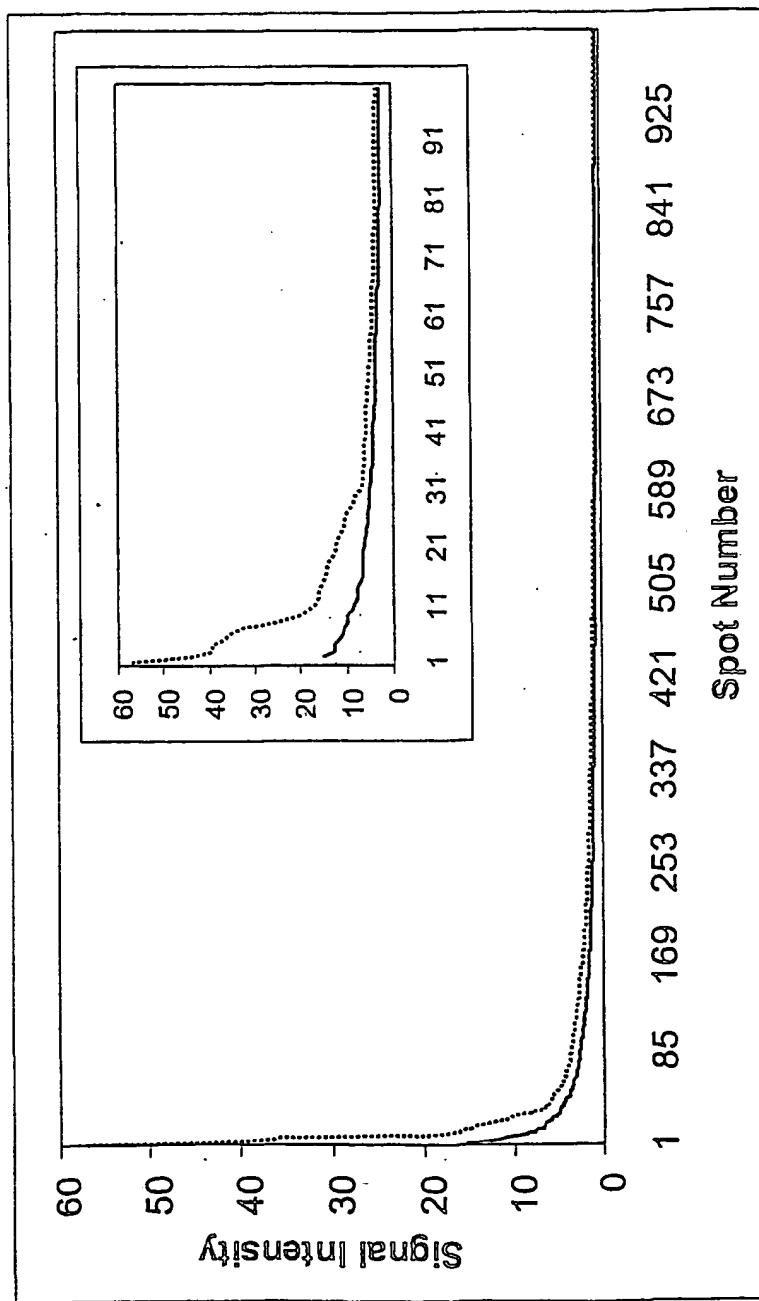


Fig. 8

9/10

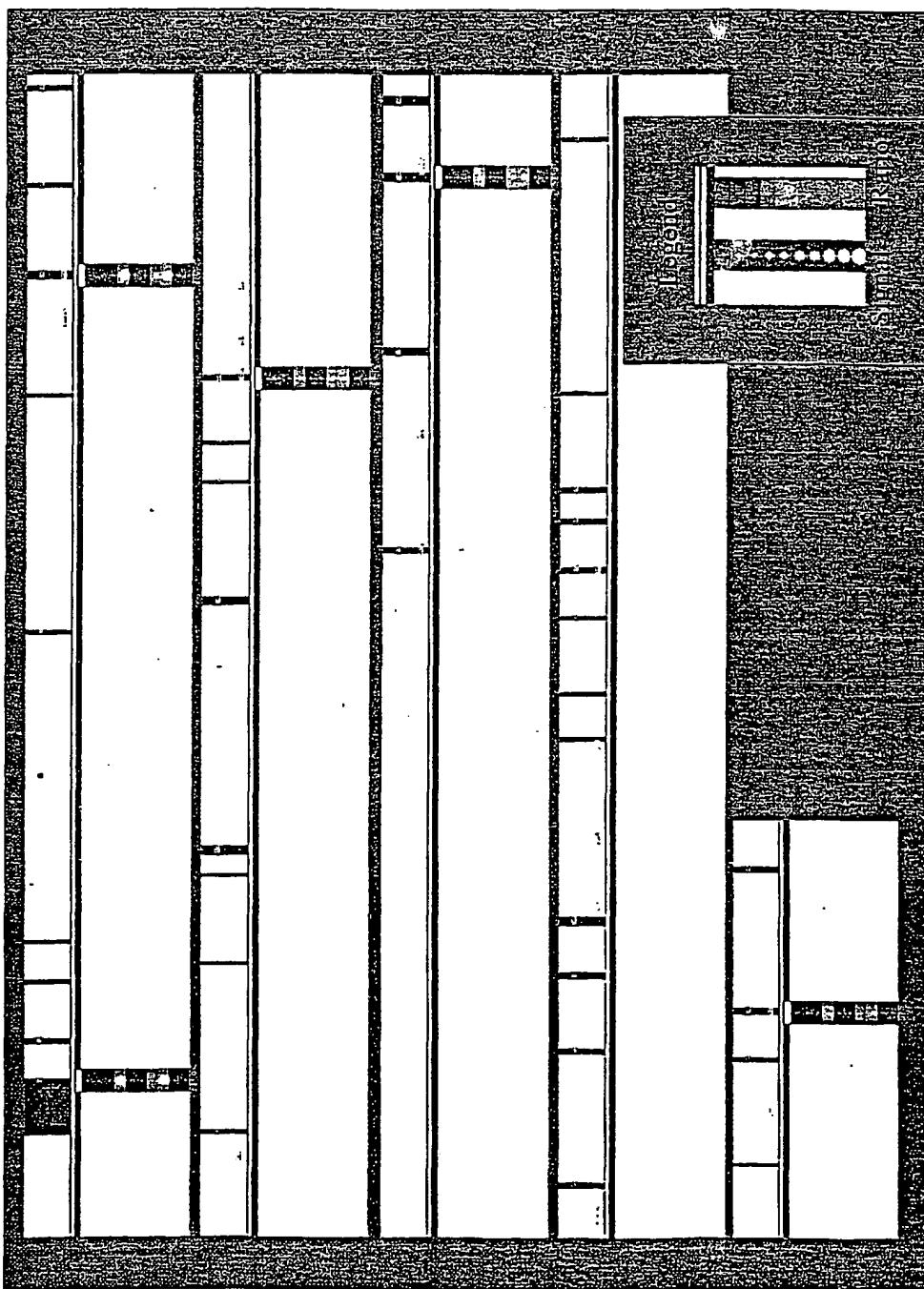


Fig. 9

10/10

Fig. 10

